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(21) International Application Number: PCT/IB98/00962 (22) International Filing Date: 22 June 1998 (22.06.98) (30) Priority Data: 60/050,380 20 June 1997 (20.06.97) US (71) Applicant (for all designated States except US): INSTITUT PASTEUR [FR/FR]; 28, rue du Docteur Roux, F-75015 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): EL SOLH, Névine [FR/FR]; 62, avenue Aubert, f-94300 Vincennes (FR). ALLIGNET, Jeanine [FR/FR]; 38, rue Salvadore Allende, F-92000 Nanterre (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 15 April 1999 (15.04.99)	

(54) Title: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED COMPOUNDS**(57) Abstract**

The present invention pertains to polynucleotides derived from *staphylococcal* genes encoding resistance to streptogramin A or to streptogramin B and chemically related compounds. This invention also relates to the use of the polynucleotides as oligonucleotide primers or probes for detecting *Staphylococcal* strains that are resistant to streptogramin A or to streptogramin B and related compounds in a biological sample. In another embodiment, the present invention is directed to the full length coding sequences of the *staphylococcal* genes encoding for resistance to streptogramin A or to streptogramin B from *Staphylococcus* and to the polypeptides expressed by these full length coding sequences. Further, this invention relates to the use of the expressed polypeptides to produce specific monoclonal or polyclonal antibodies that serve as detection means in order to characterize any *staphylococcal* strain carrying genes encoding resistance to streptogramin A or to streptogramin B.

POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE TO
STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
COMPOUNDS

The present invention pertains to polynucleotides derived from *staphylococcal*
5 genes encoding resistance to streptogramin A or to streptogramin B and chemically
related compounds. This invention also relates to the use of the polynucleotides as
oligonucleotide primers or probes for detecting *Staphylococcal* strains that are resistant
to streptogramin A or to streptogramin B and related compounds in a biological sample.

In another embodiment, the present invention is directed to the full length coding
10 sequences of the *staphylococcal* genes encoding for resistance to streptogramin A or to
streptogramin B from *Staphylococcus* and to the polypeptides expressed by these full
length coding sequences.

Further, this invention relates to the use of the expressed polypeptides to produce
specific monoclonal or polyclonal antibodies that serve as detection means in order to
15 characterize any *staphylococcal* strain carrying genes encoding resistance to
streptogramin A or to streptogramin B.

The present invention is also directed to diagnostic methods for detecting specific
strains of *Staphylococcus* expected to be contained in a biological sample. The diagnostic
methods use the oligonucleotide probes and primers as well as the antibodies of the
20 invention.

Streptogramins and related compounds (antibiotics) produced by streptomycetes
can be classified as A and B compounds according to their basic primary structures
(Cocito, 1979). Compounds of the A group, including streptogramin A (SgA),
pristinamycin IIA (PIIA), virginiamycin M, mikamycin A, or synergistin A, are
25 polyunsaturated cyclic macrolactones. Compounds of the B group, including
streptogramin B (SgB), pristinamycin B (PIB), virginiamycin S, mikamycin B, and
synergistin B, are cyclic peptidic macrolactones (Cocito, 1979). Compounds of both
groups, A and B, bind different targets in the peptidyltransferase domain of the 50S

ribosomal subunit and inhibit protein elongation at different steps (Aumercier et al., 1992; Di Giambattista et al., 1989).

A decrease in the dissociation constant of PIB is observed in the presence of PIIA because this latter antibiotic provokes a conformational modification of the bacterial
5 ribosome at the binding sites of these molecules. Thus, A and B compounds, which are bacteriostatic when used separately, act synergistically when combined and become bactericidal, mainly against Gram-positive bacteria.

Natural mixtures such as pristinamycin (Pt), synergistin, virginiamycin and mikamycin, are used orally and topically. A semi-synthetic injectable streptogramin,
10 RP59500, consisting of a mixture of derivatives of A and B compounds (Dalfopristin and Quinupristin, respectively) is currently undergoing *in vivo* experimental and clinical trials (J. Antimicrob. Agents Chemother. 30 (Suppl. A), entire volume, 1992; Entenza et al., 1995; Fantin et al., 1995; Griswold et al., 1996; Torralba et al., 1995). Staphylococcal resistance to synergistic mixtures of A and B compounds (Pt MIC $\geq 2 \mu\text{g/ml}$) is always
15 associated with resistance to A compounds (PIIA MIC $\geq 8 \mu\text{g/ml}$), but not necessarily with resistance to B compounds (Allignet et al., 1996).

To date, four genes encoding resistance to A compounds have been isolated from staphylococcal and enterococcal plasmids. The genes *vat* (Allignet et al., 1993), *vatB* (Allignet and El Solh, 1995), and *satA* (Rende-Fournier et al., 1993) encode related
20 acetyltransferases (50.4-58.3 % amino acids), which inactivate streptogramin A and similar compounds. The staphylococcal gene *vga* (Allignet et al., 1992) encodes an ATP-binding protein probably involved in the active efflux of A compounds. Nevertheless, there continues to exist a need in the art for polynucleotides specific for *Staphylococcus* resistant to streptogramin A and/or B and related compounds.

25

SUMMARY OF THE INVENTION

Accordingly, this invention aids in fulfilling this need in the art. In particular, this invention provides a purified peptide comprising an amino acid sequence selected from the group consisting of :

- 5 a) SEQ ID NO: 4 which corresponds to the complete amino acid sequence of Vga B or fragments derived from SEQ ID NO: 4 containing at least 10 amino acids;
- b) SEQ ID NO: 5 which corresponds to the complete amino acid sequence of Vat C or fragments derived from SEQ ID NO: 5 containing at least 10 amino acids;
- 10 c) SEQ ID NO: 6 which corresponds to the complete amino acid sequence of Vgb B or fragments derived from SEQ ID NO: 6 containing at least 10 amino acids;
- d) SEQ ID NO: 7 which corresponds to the complete amino acid sequence of Vgb B;
- 15 e) SEQ ID NO: 8 which corresponds to a fragment of the amino acid sequence of Vga B;
- f) SEQ ID NO: 9 which corresponds to a fragment of the amino acid sequence of Vat C; and
- g) SEQ ID NO: 10 which corresponds to a fragment of the amino acid sequence of Vat C.

This invention additionally provides a purified polynucleotide comprising the nucleotide sequence selected from the group consisting of :

- a) SEQ ID NO: 1 which corresponds to the complete nucleic acid sequence of vga B or fragments derived from SEQ ID NO: 1 containing 15 to 40 nucleotides;
- 25 b) SEQ ID NO: 2 which corresponds to the complete nucleic acid sequence of vat C or fragments derived from SEQ ID NO: 2 containing 15 to 40 nucleotides;
- c) SEQ ID NO: 3 which corresponds to the complete nucleic acid sequence of vgb B or fragments derived from SEQ ID NO: 3 containing 15 to 40 nucleotides;

d) SEQ ID NO: 11 which corresponds to the nucleic acid sequence encoding the polypeptide of SEQ ID NO: 7;

e) SEQ ID NO: 12 which corresponds to the nucleic acid sequence encoding the polypeptide of SEQ ID NO: 8 ;

5 f) SEQ ID NO: 13 which corresponds to the nucleic acid sequence encoding the polypeptide of SEQ ID NO: 9; and

g) SEQ ID NO: 14 which corresponds to the nucleic acid sequence encoding the polypeptide of SEQ ID NO: 10.

Furthermore, this invention includes a purified peptide comprising the amino acid
10 sequence encoded by the nucleotide sequence selected from the group consisting of :

a) SEQ ID NO: 1,

b) SEQ ID NO: 2,

c) SEQ ID NO: 3,

d) SEQ ID NO: 11,

15 e) SEQ ID NO: 12,

f) SEQ ID NO: 13, and

g) SEQ ID NO: 14.

This invention also provides a composition comprising purified polynucleotide sequences including at least one nucleotide sequence selected from the group consisting
20 of polynucleotides, genes or cDNA of *vgaB*, *vatC*, and *vgbB*, which are useful for the detection of resistance to streptogramin A and/or to streptogramin B and related compounds. This invention further provides a composition comprising purified amino acid sequences including at least an amino acid sequence from a polypeptide encoded by a polynucleotide selected from the group consisting of polynucleotides, genes or cDNA of
25 *vgaB*, *vatC*, and *vgbB*, which are useful for the detection of resistance to streptogramin A and/or to streptogramin B and related compounds.

In another embodiment, this invention provides a composition of polynucleotide sequences encoding resistance to streptogramins and related compounds, or inducing this resistance in Gram-positive bacteria, wherein the composition comprises a combination of at least two of the following nucleotide sequences: a) a nucleotide sequence encoding an acetyltransferase conferring resistance to streptogramin A and related compounds, b) a nucleotide sequence encoding a molecule containing ATP binding motifs conferring resistance to streptogramin A and related compounds; and c) a nucleotide sequence encoding a lactonase conferring resistance to streptogramin B and related compounds.

Furthermore, this invention provides a composition of polynucleotide sequences, wherein the sequence encoding a molecule containing ATP binding motifs confers resistance to *Staphylococci* and particularly to *S. aureus*, and wherein the polynucleotide sequence corresponds to a *vgaB* nucleotide sequence represented by SEQ ID NO: 1 or a sequence having at least 70% homology with *vgaB* complete nucleotide sequence, or to a polynucleotide hybridizing with SEQ ID NO: 1 under stringent conditions, or to a fragment containing between 20 and 30 nucleotides of SEQ ID NO: 11 or SEQ ID NO: 12, or wherein the polynucleotide sequence encodes a polypeptide having at least 60% homology with the complete SEQ ID NO: 4 or with SEQ ID NO: 7 or SEQ ID NO: 8.

Furthermore this invention relates to a composition of polynucleotide sequences, wherein the sequence encoding an acetyltransferase confers resistance to streptogramin A and related compounds in *Staphylococci*, and particularly in *S. cohnii*, and wherein the polynucleotide sequence corresponds to a *vatC* nucleotide sequence represented by SEQ ID NO: 2 or a sequence having at least 70% homology with *vatC* complete nucleotide sequence, or to a polynucleotide hybridizing with SEQ ID NO: 2 under stringent conditions, or to a fragment containing between 20 and 30 nucleotides of SEQ ID NO: 13 or SEQ ID NO: 14, or wherein the polynucleotide sequence encodes a polypeptide having at least 60% homology with the complete SEQ ID NO: 5 or with SEQ ID NO: 9 or SEQ ID NO: 10.

This invention also provides a composition of polynucleotide sequences, wherein the sequence encoding a lactonase confers resistance to streptogramin B and related compounds in *Staphylococci* and particularly in *S. cohnii*, and wherein the polynucleotide sequence corresponds to a *vgbB* nucleotide sequence represented in SEQ ID NO: 3 or
5 a sequence having at least 70% homology with *vgbB* complete nucleotide sequence, or to a polynucleotide hybridizing with SEQ ID NO: 3 under stringent conditions, or to a fragment containing between 20 and 40 nucleotides of SEQ ID NO: 3, or wherein the polynucleotide sequence encodes a polypeptide having at least 60% homology with the complete SEQ ID NO: 6.

10 The invention also contemplates a composition of polynucleotide sequences, wherein at least a *valB* nucleotide sequence encoding an acetyltransferase conferring resistance to streptogramin A and related compounds is included in addition to a *vgaB* nucleotide sequence encoding a molecule containing ATP binding motifs conferring resistance to streptogramin A.

15 Additionally, the invention includes a purified polynucleotide that hybridizes specifically under stringent conditions with a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14.

20 The invention further includes polynucleotide fragments comprising at least 10 nucleotides capable of hybridization under stringent conditions with any one of the nucleotide sequences enumerated above.

In another embodiment of the invention, a recombinant DNA sequence comprising at least one nucleotide sequence enumerated above and under the control of regulatory elements that regulate the expression of resistance to antibiotics of the
25 streptogramin family in a defined host is provided.

Furthermore, the invention includes a recombinant vector comprising the recombinant DNA sequence noted above, wherein the vector comprises the plasmid pIP1633 or plasmid pIP1714.

The invention also includes a recombinant cell host comprising a polynucleotide sequence enumerated above or the recombinant vector defined above.

In still a further embodiment of the invention, a method of detecting bacterial strains that contain the polynucleotide sequences set forth above is provided.

5 Additionally, the invention includes kits for the detection of the presence of bacterial strains that contain the polynucleotide sequences set forth above.

The invention also contemplates antibodies recognizing peptide fragments or polypeptides encoded by the polynucleotide sequences enumerated above.

10 Still further, the invention provides for a screening method for active antibiotics and/or molecules for the treatment of infections due to Gram-positive bacteria, particularly staphylococci, based on the detection of activity of these antibiotics and/or molecules on bacteria having the resistance phenotype to streptogramins.

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive
15 of the invention, as claimed.

BRIEF DESCRIPTION OF THE DRAWINGS

This invention will be more fully described with reference to the drawings in which:

20 FIG. 1A and 1B are the restriction maps of the 5.5 kb *Bg*/II fragment and of the 2.4 kb *Hind*III-*Hae*III fragment of pIP1633, respectively. Both fragments confer resistance to streptogramin A and related compounds. The strategy for sequencing the 2.4 kb *Hind*III-*Hae*III fragment is given in Fig. 1B. Restriction enzyme abbreviations: Ba, *Bam*HI; Bg, *Bg*/II; E, *Eco*RI; H, *Hind*III; X, *Xba*I.

25 FIG. 2 is the nucleotide sequence and deduced amino acid sequence of 2411 nucleotides from pIP1633, which contains the gene *vgaB* of *S. aureus* conferring resistance to streptogramin A and related compounds. The putative ribosome binding site (RBS) is underlined. The amino acids are aligned with the second nucleotide of each

codon. Asterisks indicate the in-frame stop codons. The A and B ATP-binding motifs described by Walker et al. (1982) and detected within each of the two ATP-domains are boxed. The conserved motif SGG of the two copies of loop 3 described by Hyde et al. (1990) is underlined. Relevant restriction sites are shown.

5 FIG. 3 is the amino acid sequence alignment of the predicted 60 and 61 kDa proteins encoded by Vga (Allignet et al., 1992, accession No: m90056) and VgaB (FIG.2), respectively. Identical residues are indicated by asterisks and conservative changes are shown by single dots. The A and B motifs of Walker et al. (1982) are in bold type (WA, WB). The conserved motif SGG of the two copies of loop 3 described by
10 Hyde et al. (1990) is underlined.

FIG. 4 is a restriction map of the plasmid pIP1714 carrying the genes *vatC* and *vgbB* as well as the genes *pre* and *repB* of *S. cohnii* strain BM10711 resistant to the synergistic mixtures of streptogramins A and B.

15 FIG. 5 is the nucleotide sequence and deduced amino acid sequence of 1727 nucleotide from pIP1714, which contains the gene *vgbB* and *vatC* of *S. cohnii*. Relevant restriction sites are shown.

FIG. 6 A, 6B, and 6C represent oligonucleotide primers for hybridization under stringent conditions with *vatC*, *vgbB*, and *vgaB* respectively.

FIG. 7 represents SEQ ID NOs: 1-14.

20

DETAILED DESCRIPTION OF THE INVENTION

It has now been determined that bacteria from the *Staphylococcus* genus carry a *vgaB* gene, which encodes a putative ATP-binding protein that confers resistance to streptogramin A and structurally similar compounds. It has also now been determined
25 that bacteria from the *Staphylococcus* genus carry a *vgbB* gene, which encodes a lactonase that confers resistance to streptogramin B and structurally similar compounds, and a *vatC* gene, which encodes an acetyltransferase that confers resistance to streptogramin A and structurally similar compounds.

Novel polynucleotides corresponding to the *vgaB*, *vgbB*, and *vatC* genes from various strains of *Staphylococcus* have been isolated and sequenced, and it has been surprisingly demonstrated that these new polynucleotides make it possible to design oligonucleotide probes or primers. These polynucleotides include the following:

- 5 a) SEQ ID NO: 1,
 b) SEQ ID NO: 2,
 c) SEQ ID NO: 3,
 d) SEQ ID NO: 11,
 e) SEQ ID NO: 12,
10 f) SEQ ID NO: 13, and
 g) SEQ ID NO: 14.

This invention provides specific pairs of oligonucleotide primers or probes that hybridize specifically, under stringent hybridization conditions as defined hereinafter, to the nucleic acid (RNA or DNA) from a particular strain of the *Staphylococcus* genus.

15 These oligonucleotide primers include the following:

- a) Oligo I 5'-AAGTCGACTGACAATATGAGTGGTGG-3'
 Oligo II 5'-CTGCAGATGCCTCAACAGCATCGATATCC-3'
 b) Oligo III 5'- ATGAATTCGCAAATCAGCAAGG -3'
 Oligo IV 5'- TCGTCTCGAGCTCTAGGTCC -3'
20 c) Oligo V 5'- CAGCAGTCTAGATCAGAGTGG -3'
 Oligo VI 5'- CATACGGATCCACCTTTTCC -3'.

In a specific embodiment of the present invention, the purified polynucleotides useful for detecting *Staphylococcal* strains can be used in combination in order to detect bacteria belonging to *Staphylococci* in a biological sample. Thus, the present invention
25 also provides detection methods and kits comprising combinations of the purified polynucleotides according to the invention. The purified oligonucleotides of the invention are also useful as primers for use in amplification reactions or as nucleic acid probes.

By "polynucleotides" according to the invention is meant the sequences referred to as SEQ ID NOs: 1, 2, 3, OR 11, 12, 13, 14 and the complementary sequences and/or the sequences of polynucleotides which hybridize to the referred sequences in high stringent conditions and which are used for detecting *staphylococcal* strains carrying a gene encoding resistance to streptogramin A or to streptogramin B.

By "active molecule" according to the invention is meant a molecule capable of inhibiting the activity of the purified polypeptide as defined in the present invention or capable of inhibiting the bacterial culture of *staphylococcal* strains.

Thus, the polynucleotides of SEQ ID NOs: 1-3 and 11-14 and their fragments can be used to select nucleotide primers notably for an amplification reaction, such as the amplification reactions further described.

PCR is described in the U.S. Patent No. 4,683,202 granted to Cetus Corp. The amplified fragments may be identified by agarose or polyacrylamide gel electrophoresis, or by a capillary electrophoresis, or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography, or ion exchange chromatography). The specificity of the amplification can be ensured by a molecular hybridization using as nucleic probes the polynucleotides of SEQ ID NOs: 1-3 and 11-14 and their fragments, oligonucleotides that are complementary to these polynucleotides or fragments thereof, or their amplification products themselves.

Amplified nucleotide fragments are useful as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the present invention or in order to detect the presence of a bacteria of *Staphylococcal* strain carrying genes encoding resistance to streptogramin A or streptogramin B, in a biological sample. This invention also provides the amplified nucleic acid fragments ("amplicons") defined herein above. These probes and amplicons can be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

Preferred nucleic acid fragments that can serve as primers according to the present invention are the following:

polynucleotides of sequence SEQ ID NOs: 1-3 and 11-14; and
polynucleotides having a length from 20 to 30 consecutive
nucleotides from a polynucleotide selected from the group consisting of
polynucleotides of sequences SEQ ID NO: 11 to SEQ ID NO: 14 or from
5 20 to 40 consecutive nucleotides from a polynucleotide of SEQ ID NO:
3

The primers can also be used as oligonucleotide probes to specifically detect a
polynucleotide according to the invention.

Other techniques related to nucleic acid amplification can also be used and are
10 generally preferred to the PCR technique. The Strand Displacement Amplification (SDA)
technique (Walker et al., 1992) is an isothermal amplification technique based on the
ability of a restriction enzyme to cleave one of the strands at a recognition site (which is
under a hemiphosphorothioate form), and on the property of a DNA polymerase to
initiate the synthesis of a new strand from the 3' OH end generated by the restriction
15 enzyme and on the property of this DNA polymerase to displace the previously
synthesized strand being localized downstream.

The SDA amplification technique is more easily performed than PCR (a single
thermostated water bath device is necessary), and is faster than the other amplification
methods. Thus, the present invention also comprises using the nucleic acid fragments
20 according to the invention (primers) in a method of DNA or RNA amplification according
to the SDA technique. The polynucleotides of SEQ ID NOs: 1-3 and 11-14 and
their fragments, especially the primers according to the invention, are useful as technical
means for performing different target nucleic acid amplification methods such as:

- 25 - TAS (Transcription-based Amplification System), described by Kwoh et al. in
1989;
- SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990;
- NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et
al. in 1991; and

- TMA (Transcription Mediated Amplification).

The polynucleotides of SEQ ID NOs: 1-3 and 11-14 and their fragments, especially the primers according to the invention, are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe,

5 such as:

- LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991, who employ a thermostable ligase;

- RCR (Repair Chain Reaction), described by Segev et al. in 1992;

- CPR (Cycling Probe Reaction), described by Duck et al. in 1990; and

10 - Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988, and by Burg et al. and Stone et al. in 1996.

When the target polynucleotide to be detected is RNA, for example mRNA, a reverse transcriptase enzyme can be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA
15 can be subsequently used as the nucleic acid target for the primers or the probes used in an amplification process or a detection process according to the present invention.

Nucleic probes according to the present invention are specific to detect a polynucleotide of the invention. By "specific probes" according to the invention is meant any oligonucleotide that hybridizes with one polynucleotide of SEQ ID NOs: 1-3 and 11-
20 14 and which does not hybridize with unrelated sequences. Preferred oligonucleotide probes according to the invention are oligonucleotides I-VI.

In a specific embodiment, the purified polynucleotides according to the present invention encompass polynucleotides having at least 80% homology in their nucleic acid sequences with polynucleotides of SEQ ID NO: 11 to SEQ ID NO: 14, at least 70%
25 identity with SEQ ID NO: 1 to 3. By percentage of nucleotide homology according to the present invention is intended a percentage of identity between the corresponding bases of two homologous polynucleotides, this percentage of identity being purely statistical

and the differences between two homologous polynucleotides being located at random and on the whole length of said polynucleotides.

The oligonucleotide probes according to the present invention hybridize specifically with a DNA or RNA molecule comprising all or part of one polynucleotide among SEQ ID NOs: 1-3 and 11-14 under stringent conditions. As an illustrative embodiment, the stringent hybridization conditions used in order to specifically detect a polynucleotide according to the present invention are advantageously the following:

Prehybridization and hybridization are performed at 68°C in a mixture containing:

- 5X SSPE (1X SSPE is .3 M NaCl, 30 mM tri-sodium citrate
- 5X Denhardt's solution
- 0.5% (w/v) sodium dodecyl sulfate (SDS); and
- 100 µg ml⁻¹ salmon sperm DNA

The washings are performed as follows:

- Two washings at laboratory temperature for 10 min. in the presence of 2 x SSPE and 0.1 % SDS;
- One washing at 68°C for 15 min. in the presence of 1 x SSPE, .1% SDS; and
- One washing at 68°C for 15 min. in the presence of 0.1 x SSPE and 0.1 % SDS.

The non-labeled polynucleotides or oligonucleotides of the invention can be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides are generally labeled with a radioactive element (³²P, ³⁵S, ³H, ¹²⁵I) or by a non-isotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5-bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

Examples of non-radioactive labeling of nucleic acid fragments are described in the French Patent No. FR 78 10975 or by Urdea et al. or Sanchez-Pescador et al. 1988.

Other labeling techniques can also be used, such as those described in the French patents 2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al. 1988). A general method comprises immobilizing the nucleic acid that has been extracted from the biological sample on a substrate (nitrocellulose, nylon, polystyrene) and then incubating, in defined conditions, the target nucleic acid with the probe. Subsequent to the hybridization step, the excess amount of the specific probe is discarded, and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence, or enzyme activity measurement).

Advantageously, the probes according to the present invention can have structural characteristics such that they allow signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European Patent No. 0 225 807 (Chiron).

In another advantageous embodiment of the present invention, the probes described herein can be used as "capture probes", and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe, which recognizes a sequence of the target nucleic acid that is different from the sequence recognized by the capture probe.

The oligonucleotide fragments useful as probes or primers according to the present invention can be prepared by cleavage of the polynucleotides of SEQ ID NOs: 1-3 and 11-14 by restriction enzymes, as described in Sambrook et al. in 1989. Another appropriate preparation process of the nucleic acids of the invention containing at most 200 nucleotides (or 200 bp if these molecules are double-stranded) comprises the following steps:

- synthesizing DNA using the automated method of beta-cyanethylphosphoramidite described in 1986;
 - cloning the thus obtained nucleic acids in an appropriate vector;
- and

- purifying the nucleic acid by hybridizing to an appropriate probe according to the present invention.

A chemical method for producing the nucleic acids according to the invention, which have a length of more than 200 nucleotides (or 200 bp if these molecules are
5 double-stranded), comprises the following steps:

- Assembling the chemically synthesized oligonucleotides having different restriction sites at each end;

- cloning the thus obtained nucleic acids in an appropriate vector;

and

10 - purifying the nucleic acid by hybridizing to an appropriate probe according to the present invention.

The oligonucleotide probes according to the present invention can also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of one or several bases,
15 one from the other, each probe of the matrix library thus being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix can be a material able to act as an electron donor, the detection of the matrix positions in which hybridization has occurred being subsequently determined by an electronic device.

Such matrix libraries of probes and methods of specific detection of a target nucleic acid
20 are described in the European patent application No. 0 713 016, or PCT Application No. WO 95 33846, or also PCT Application No. WO 95 11995 (Affymax Technologies), PCT Application No. WO 97 02357 (Affymetrix Inc.), and also in U.S. Patent No. 5,202,231 (Drmanac), said patents and patent applications being herein incorporated by reference.

The present invention also pertains to a family of recombinant plasmids containing
25 at least a nucleic acid according to the invention. According to an advantageous embodiment, a recombinant plasmid comprises a polynucleotide of SEQ ID NOs: 1-3 and 11-14 or one nucleic fragment thereof. More specifically, the following plasmids are part of the invention: pIP1633 and pIP1714.

The present invention is also directed to the full length coding sequences of the *vgaB*, *vgbB*, and *vatC* genes from *Staphylococci* that are available using the purified polynucleotides according to the present invention, as well as to the polypeptide enzymes encoded by these full length coding sequences. In a specific embodiment of the present invention, the full length coding sequences of the *vgaB*, *vgbB*, and *vatC* genes are isolated from a plasmid or cosmid library of the genome of *Staphylococci* that have been screened with the oligonucleotide probes according to the present invention. The selected positive plasmid or cosmid clones hybridizing with the oligonucleotide probes of the invention are then sequenced in order to characterize the corresponding full length coding sequence, and the DNA insert of interest is then cloned in an expression vector in order to produce the corresponding ATP binding motif conferring resistance to streptogramin A and related compounds, acetyltransferase conferring resistance to streptogramin A and related compounds, or lactonase conferring resistance to streptogramin B and related compounds.

A suitable vector for the expression in bacteria and in particular in *E. coli*, is the pQE-30 vector (QIAexpress) that allows the production of a recombinant protein containing a 6xHis affinity tag. The 6xHis tag is placed at the C-terminus of the recombinant polypeptide ATP binding motif conferring resistance to streptogramin A and related compounds, acetyltransferase conferring resistance to streptogramin A and related compounds or lactonase conferring resistance to streptogramin B and related compounds, which allows a subsequent efficient purification of the recombinant polypeptide ATP binding motif conferring resistance to streptogramin A and related compounds, acetyltransferase conferring resistance to streptogramin A and related compounds, or lactonase conferring resistance to streptogramin B and related compounds by passage onto a nickel or copper affinity chromatography column. The nickel chromatography column can contain the Ni-NTA resin (Porath et al. 1975).

The polypeptides according to the invention can also be prepared by conventional methods of chemical synthesis, either in a homogenous solution or in solid phase. As an

illustrative embodiment of such chemical polypeptide synthesis techniques the homogenous solution technique described by Houbenweyl in 1974 may be cited.

The polypeptides according to the invention can be characterized by binding onto an immunoaffinity chromatography column on which polyclonal or monoclonal antibodies
5 directed to a polypeptide among the ATP binding motif conferring resistance to streptogramin A and related compounds, acetyltransferase conferring resistance to streptogramin A and related compounds, or lactonase conferring resistance to streptogramin B and related compounds of the invention have previously been immobilized.

10 Another object of the present invention comprises a polypeptide produced by the genetic engineering techniques or a polypeptide synthesized chemically as above described.

The polypeptide ATP binding motif conferring resistance to streptogramin A and related compounds, acetyltransferase conferring resistance to streptogramin A and related
15 compounds, or lactonase conferring resistance to streptogramin B and related compounds according to the present invention are useful for the preparation of polyclonal or monoclonal antibodies that recognize the polypeptides or fragments thereof. The monoclonal antibodies can be prepared from hybridomas according to the technique described by Kohler and Milstein in 1975. The polyclonal antibodies can be prepared by
20 immunization of a mammal, especially a mouse or a rabbit, with a polypeptide according to the invention that is combined with an adjuvant, and then by purifying specific antibodies contained in the serum of the immunized animal on a affinity chromatography column on which has previously been immobilized the polypeptide that has been used as the antigen.

25 Consequently, the invention is also directed to a method for detecting specifically the presence of a polypeptide according to the invention in a biological sample. The method comprises:

- a) bringing into contact the biological sample with an antibody according to the invention; and
- b) detecting antigen-antibody complex formed.

Also part of the invention is a diagnostic kit for *in vitro* detecting the presence of
5 a polypeptide according to the present invention in a biological sample. The kit comprises:

- a polyclonal or monoclonal antibody as described above, optionally labeled; and
- a reagent allowing the detection of the antigen-antibody
10 complexes formed, wherein the reagent carries optionally a label, or being able to be recognized itself by a labeled reagent, more particularly in the case when the above-mentioned monoclonal or polyclonal antibody is not labeled by itself.

15 Indeed, the monoclonal or polyclonal antibodies according to the present invention are useful as detection means in order to identify or characterize a *Staphylococcal* strain carrying genes encoding resistance to streptogramin A or streptogramin B.

The invention also pertains to:

20 A purified polypeptide or a peptide fragment having at least 10 amino acids, which is recognized by antibodies directed against a polynucleotide sequence conferring resistance to streptogramin and related compounds, corresponding to a polynucleotide sequence according to the invention.

A polynucleotide comprising the full length coding sequence of a *Staphylococcus*
25 streptogramin A and/or B resistant gene containing a polynucleotide sequence according to the invention.

A monoclonal or polyclonal antibody directed against a polypeptide or a peptide fragment encoded by the polynucleotide sequences according to the invention.

A method of detecting the presence of bacterium harboring the polynucleotide sequences according to the invention in a biological sample comprising:

- a) contacting bacterial DNA of the biological sample with a primer or a probe according to the invention, which hybridizes with a nucleotide sequence encoding resistance to streptogramins;
- b) amplifying the nucleotide sequence using said primer or said probe; and
- c) detecting the hybridized complex formed between said primer or probe with the DNA.

A kit for detecting the presence of bacterium having resistance to streptogramin A and/or streptogramin B and harboring the polynucleotide sequences according to the invention in a biological sample, said kit comprising:

- a) a polynucleotide probe according to the invention; and
- b) reagents necessary to perform a nucleic acid hybridization reaction.

A kit for detecting the presence of bacterium having resistance to streptogramin A and harboring the polynucleotide sequences according to the invention in a biological sample, said kit comprising:

- a) a polynucleotide probe according to the invention; and
- b) reagents necessary to perform a nucleic acid hybridization reaction.

A method of screening active antibiotics for the treatment of the infections due to Gram-positive bacteria, comprising the steps of:

- a) bringing into contact a Gram-positive bacteria having a resistance to streptogramin A or streptogramin B and related compounds and containing the polynucleotide sequences according to the invention with the antibiotic; and

- b) measuring an activity of the antibiotic on the bacteria having a resistance to streptogramins and related compounds.

A method of screening for active synthetic molecules capable of penetrating into a bacteria of the family of staphylococci, wherein the inhibiting activity of these molecules is tested on at least a polypeptide encoded by the polynucleotide sequences according to the invention comprising the steps of:

- a) contacting a sample of said active molecules with the bacteria;
- b) testing the capacity of the active molecules to penetrate into the bacteria and the capacity of inhibiting a bacterial culture at various concentration of the molecules; and
- c) choosing the active molecule that provides an inhibitory effect of at least 80% on the bacterial culture compared to an untreated culture.

An *in vitro* method of screening for active molecules capable of inhibiting a polypeptide encoded by the polynucleotide sequences according to the invention, wherein the inhibiting activity of these molecules is tested on at least said polypeptide, said method comprising the steps of:

- a) extracting a purified polypeptide according to the invention;
- b) contacting the active molecules with said purified polypeptide;
- c) testing the capacity of the active molecules, at various concentrations, to inhibit the activity of the purified polypeptide; and
- d) choosing the active molecule that provides an inhibitory effect of at least 80 % on the activity of the said purified polypeptide.

A composition of a polynucleotide sequence encoding resistance to streptogramins and related compounds, or inducing resistance in Gram-positive bacteria, wherein said composition comprises a nucleotide sequence corresponding to the resistance phenotype of the plasmid pIP1633 deposited with the C.N.C.M. under the
5 Accession No. I-1768 and of the plasmid pIP1680 deposited with the C.N.C.M. under the Accession No. I-1767 and of the plasmid pIP1714 deposited with the C.N.C.M. under the number I-1877 on June 18, 1997.

A method of detecting the presence of bacterium harboring the polynucleotide sequences according to the invention in a biological sample, said method comprising the
10 steps of:

- a) contacting said sample with an antibody according to the invention that recognizes a polypeptide encoded by said polynucleotide sequences; and
- b) detecting said complex.

15 A diagnostic kit for *in vitro* detecting the presence of bacterium harboring the polynucleotide sequences according to the invention in a biological sample, said kit comprising:

- a) a predetermined quantity of monoclonal or polyclonal antibodies according to the invention;
- 20 b) reagents necessary to perform an immunological reaction between the antibodies and a polypeptide encoded by said polynucleotide sequences; and
- c) reagents necessary for detecting said complex between the antibodies and the polypeptide encoded by said polynucleotide
25 sequences.

The inhibiting activity of the molecules can be readily evaluated by one skilled in the art. For example, the inhibiting activity of Vga B can be tested by detecting its ATP hydrolysis as described in J.I. Ross et al. (1990), Mol. Microbiol. 4(7):1207-1214

regarding the rate evaluation of the active efflux of antibiotics from a cell. Ross et al. use a different gene, but their gene product functions as a drug efflux pump in the same way as Vga B does.

5 The inhibiting activity of Vat C can be tested by visualizing the acetylation reaction as described in Allignet et al. (1993) regarding the mechanism of inactivation of A-type compounds conferred by plasmids pIP680 and pIP1156 by thick layer chromatography and NMR.

10 The inhibiting activity of Vgb B can be tested by detecting the degradation of streptogramin B or a related compound by a microbiological test as described in Allignet et al. (1988).

Plasmids containing the polynucleotides from *Staphylococci*, which confer streptogramin A and/or B resistance, are referred to herein by the following accession numbers:

	<u>Plasmid</u>	<u>Accession No.</u>
15	pIP1714	I- 1877
	pIP1633	I-1768
	pIP680	I-1767

20 and they have been inserted into vectors which have been deposited at the Collection Nationale de Cultures de Microorganismes ("C.N.C.M.") Institut Pasteur, 28, rue du Docteur Roux, F-75724 Paris Cedex 15, France on June 18, 1997, and August 7, 1996, respectively.

EXAMPLES

Example 1: Cloning of the *vgaB* gene carried by plasmid pIP1633

pIP1633 was isolated from a *S. aureus* transconjugant strain, BM12235, obtained from the donor wild-type *S. aureus* strain, BM3385 (Allignet and El Solh, 1995). This plasmid carried the *vatB* gene located on a 5.5 *Bgl*II fragment, but the other described streptogramin A resistant (*SgA*^r) genes were not detected either by hybridization experiments or by PCR (Allignet and El Solh, 1995). Since the gene *vga* was carried by all the tested staphylococcal plasmids containing the *vat* gene (Allignet et al., 1996), the presence of a *vga*-related gene was suspected in pIP1633. We therefore searched this gene in the recombinant plasmid, pIP1675 (Fig. 1A), containing the *vatB*-5.5 *Bgl*II fragment of pIP1633.

First, the 2.4 kb *Hind*III-*Hae*III fragment of pIP1675, which contains only 10 nucleotide from *vatB*, was inserted into plasmid pOX300, and the recombinant plasmid, pIP1717 (Fig. 1B), was introduced by electroporation into the *S. aureus* recipient, RN4220 (Kreiwirth et al., 1983). Plasmid pOX300, also named pOX7, (Dyke and Curnock, 1989), is a hybrid of pUC18 and pEI94ts and replicates in *E. coli* where it confers resistance to ampicillin and to erythromycin, and in *S. aureus* where only resistance to erythromycin is expressed. The *S. aureus* transformants selected on 10 µg/ml erythromycin were resistant to streptogramin A and related compounds (PIIA MICs = 8-16 µg/ml). Thus, the 2.4-kb *Hind*III-*Hae*III insert of pIP1717 (Fig. 1B) probably carried a streptogramin A resistance gene and was sequenced. The nucleotide (nucleotide) sequence of this fragment was determined by the dideoxy method (Sanger et al., 1977) with the reagents and the procedure recommended by the suppliers of the T⁷ sequencing kit (Pharmacia International). Arrows indicate the direction and extent of each dideoxy-sequencing reaction. (Fig. 1B).

Example 2: The nucleotide sequence of the *vgaB* gene

The strategy of sequencing on both strands is outlined in Fig. 1 and the sequence of the 2411-bp *HindIII-HaeIII* insert is given in Fig. 2. An open reading frame (ORF) of 1674 nucleotide extending from nucleotide 682 to 2356 was detected on the same strand as *vatB* (Fig. 2). The 1674 nucleotide ORF contained an ATG start codon at nucleotide 700 to 702 and was preceded by an 8 nucleotide putative RBS. The ΔG (free energy of association) of interaction of the most stable structure between this putative RBS and the 3'-terminus of the 16S rRNA (MacLaughlin et al., 1981; Moran et al., 1982) calculated according to Tinoco et al. (1973) was -79.4 kJ/mol. The sequence located between the ATG codon and the TAA stop codon at nucleotide 2356 to 2358 may encode a 552 amino acid protein of 61,327 daltons (Da). This putative gene, named *vgaB*, had 58.8 % nucleotide identity with the 1572 bp gene, *vga* (Allignet et al., 1992). The G+C content of *vgaB* (27.2 %) is similar to that of *vga* (29 %), but both values are slightly lower than those of the staphylococcal genome (32 to 36 %) (Kloos and Schleifer, 1986). The nucleotide sequence of *vgaB* has been submitted to the GenBank/EMBL data bank under accession no. u82085.

Example 3: Amino acid sequence analysis of *VgaB*

The predicted translation product of the *vgaB* gene, *VgaB*, has a calculated isoelectric point (pI) of 9.60. The hydropathy plot of the *VgaB* sequence according to the algorithm of Kyte and Doolittle (1982) indicates the protein to be hydrophilic. No similarity to known signal sequences of secreted proteins (von Heijne, 1986; Watson, 1984) was observed.

The amino acid sequence of *VgaB* was compared with the sequences available in databases (GenBank, release 97.0; EMBL, release 48; SwissProt, release 34). Significant similarity to the ATP-binding domains of numerous ATP-binding Cassette (ABC) proteins was found. The protein giving the best match was *Vga* (48.3 % identical amino acid, 70.4 % similar amino acid). *VgaB* and *Vga* each contain two ATP-binding domains sharing 38.8 % and 39.1 % identical amino acid, respectively. Each of these domains

includes the two ATP-binding motifs described by Walker et al. (1982) (Fig.2). Moreover, the highly conserved SGG sequence of loop 3 found between the two ATP-binding motifs of all investigated ATP-binding proteins (Barrasa et al., 1995; Hyde et al., 1990) was detected in Vga (Allignet et al., 1992) and VgaB (Fig. 2). According to the predicted tertiary structure of ABC model cassette, this loop would be conveniently located to interact with the cell membrane (Hyde et al., 1990). The inter-ATP-binding domain of VgaB is more rich in glutamine (11 Q in 155 amino acid total) than the rest of the sequence of the protein (11 Q/397 amino acid). In contrast, the proportion of glutamine in the inter-ATP-binding domain of Vga is similar to that in the other part of the protein (4 Q/156 amino acid and 14 Q/366 amino acid, respectively). Neither Vga nor VgaB contains hydrophobic transmembrane domains.

The ABC protein MsrA (Ross et al., 1990) is the most similar to Vga and VgaB (35.2 % and 34.4 % identical amino acid, respectively). MsrA confers resistance to erythromycin by increasing the efflux of this antibiotic and to streptogramin B by a mechanism not yet elucidated. MsrA contains two ATP-binding domains with 31.8% amino acid identity and separated by a Q-linker, but no hydrophobic stretches that might be potential membrane spanning domains. The hydrophobic proteins, which are expected to interact with MsrA, are those encoded by similar genes mapping near MsrA in two staphylococcal strains (*smpA*, *smpB*) and also those on the chromosome of the *S. aureus* recipient strain, RN4220 (*smpC*), which does not carry *msrA* (Ross et al., 1995). Ross et al. (1996) have recently reported that SmpC found in the chromosome of RN4220 is not essential for the expression of resistance to erythromycin conferred by MsrA. Thus, further experiments are required to elucidate the mechanisms of resistance conferred by *msrA*, *vga*, or *vgaB* genes.

Several ABC transporters, which do not have alternating hydrophobic domains, have been grouped in a subfamily in order to distinguish them from the members of the ABC₂ transporter subfamily, the members of which contain hydrophobic transmembrane domains (Barrasa et al., 1995; Olano et al., 1995; Peschke et al., 1995). Thus, VgaB may

be considered as a new member of the former ABC transporter subfamily. Excluding VgaB, Vga, and MsrA, most of the known ABC transporters that contain two ATP-binding cassettes but no hydrophobic domain(s) were found in lantibiotic or antibiotic producing microorganisms in which they are involved in the active excretion of these molecules. These transporters are encoded by the following genes: *ard1*, an aminoacylnucleoside antibiotic resistance gene from *Streptomyces capreolus* (Barrasa et al., 1995); *carA*, a carbomycin-resistance gene from *Streptomyces thermotolerans* (Schoner et al., 1992); *ImrC*, a lincomycin-resistance gene from *Streptomyces lincolnensis* (Peschke et al., 1995); *oleB*, an oleandomycin-resistance gene from *Streptomyces antibioticus* (Olano et al., 1995); *srmB*, a spiramycin-resistance gene from *Streptomyces ambofaciens* (Geistlich et al., 1992); *tlrC*, a tylosin-resistance gene from *Streptomyces fradiae* (Rosteck et al., 1991); and *petT*, a pep5 epidermin-resistance gene from *Staphylococcus epidermidis* (Meyer et al., 1995). The amino acid identity between each of these latter ABC transporters and VgaB is between 23.6 % and 28.7 %.

Degenerate primers designed from an analysis of the alignment of the amino acid sequence of Vga and VgaB may be helpful to detect such putative genes by PCR experiments. In the streptogramins producers, the described resistance to these antibiotics consists of streptogramin A inactivation by an as yet unknown mechanism (Fierro et al., 1989), streptogramin B inactivation by a lactonase (Kim et al., 1974) and putative increased export of streptogramin A and streptogramin B by an integral membrane protein, Ptr, exploiting transmembrane proton gradients (Blanc et al., 1995). The NMR spectra of the modified A compounds may be analyzed to verify if their inactivation in the antibiotic producers is similar to that due to the proteins Vat or VatB, which transfer an o-acetyl group to position C14 of PIIA (Allignet et al., 1993). Interestingly, the staphylococcal gene *vgb* (Allignet et al., 1988) found in most plasmids carrying *vga* and *vat* (Allignet et al., 1996), encodes a protein inactivating streptogramin B and related compounds by cleavage of the lactone ring.

Example 4: *Distribution and location of the vgaB gene in 52 SgA^R and independent wild-type staphylococci*

A recombinant plasmid containing a fragment of *vgaB*, pIP1705, was constructed to serve as a probe in hybridization experiments under stringent conditions as described previously (Allignet et al., 1996). pIP1705 consists of pUC19 cleaved with *Sal*I and *Pst*I, and an insert of 1051 bp amplified from within *vgaB* by the following primers, which introduce *Pst*I or *Sal*I sites:

Oligo I 5'-AAGTCGACTGTGACAATATGAGTGGTGG-3'

*Sal*I

Oligo II 5'-CTGCAGATGCCTCAACAGCATCGATATCC-3'

*Pst*I

The 52 SgA^R staphylococci investigated (Allignet et al., 1996; El Solh et al., 1980; Loncle et al., 1993) included 10 strains (7 *S. aureus*, 1 *S. simulans*, 1 *S. haemolyticus*, and 1 *S. cohnii urealyticum*), which harbored 26 to 45 kb plasmids containing *vga*, *vat*, and *vgb*; 21 strains (20 *S. aureus* and one *S. epidermidis*), which harbored 50 to 90 kb plasmids containing *vatB*; 16 strains (12 *S. epidermidis*, three *S. haemolyticus* and one *S. aureus*) with 6 to 15 kb plasmids containing *vga*; one *S. epidermidis* strain which harbored a plasmid of approximately 20 kb containing *vga-vat*; and four *S. aureus* strains, which do not carry nucleotide sequences hybridizing with *vat*, *vatB*, *vga*, or *vgb*. Nucleotide sequences hybridizing with pIP1705 were found only in the 21 large plasmids containing *vatB*. In all these 21 plasmids including pIP1633, the hybridizing nucleotide sequences were detected on a 1.5 kb *Eco*RI fragment, which also hybridized with *vatB*, suggesting that *vgaB* and *vatB* have conserved relative positions.

Example 5: *Results concerning vatC and vgbB genes*

The *Staphylococcus cohnii* strain, BM10711, resistant to the synergistic mixtures streptogramin A and streptogramin B and related compounds (pristinamycin, virginiamycin, synergistin, mikamycin, Quinupristin-Dalfopristin) was analyzed. This strain was isolated at Douera hospital (Algeria) where the pristinamycin was frequently used topically. The strain was isolated (Liassin et al., 1997) from a sample provided from a cupboard located in a room occupied by patients suffering from chronic osteomyelitis.

The strain BM10711 harbored several plasmids including pIP1714 (5kb). This plasmid was isolated by electroporation in a *S. aureus* recipient strain, RN4220. The transformant, harboring pIP1714, was selected on BHIA containing 10 µg/ml pristinamycin IIA. Plasmid pIP1714 conferred resistances to streptogramin A and streptogramin B and related compounds.

Plasmid pIP1714 was linearized by cleavage with *Hind*III and cloned in the *Hind*III site of the vector pOX7 also named pOX300 (Dyke et al., 1989, FEMS Microbiol. Lett. 58:209-216). pOX7 results from the cointegration of the *E. coli* vector, pUC18, and *S. aureus* plasmid, pE194. The recombinant plasmid pIP1715 consisting of pOX7 and pIP1714 was used to sequence pIP1714 in its entirety. The gene *vatC* (636 nucleotides) encoding an acetyltransferase inactivating streptogramin A and related compounds and the gene *vgbB* (885 nucleotides) encoding a lactonase inactivating streptogramin B and related compounds were found to be carried by this plasmid. The gene *vatC* had 71.7, 62.2 and 64.1 % nucleotides identity with *vat*-related gene, *vatB* and *satA* respectively and the gene *vgbB* presents 69.5 % nucleotides identity with the gene *vgb*.

VatC acetyltransferase exhibits significant similarity with acetyltransferases having the same enzymatic activity and encoded by the genes *vatC*, *vatB*, and *sat* (respectively 69.8, 58.2 and 66.0 % amino acids identity). These proteins belong to a family of xenobiotic acetyltransferases modifying various substrates including streptogramin A and

related antibiotics. VgbB lactonase exhibits as well significant similarity with Vgb inactivating streptogramin B and related (67.0 % amino acids identity).

The two other genes carried by pIP1714 are *pre* and *repB*, encoding proteins involved in mobilization and replication, respectively. These two genes are homologous to those carried by the staphylococcal plasmid, pUB110 (McKenzie et al., 1986, Plasmid 15:93-103). Moreover, as reported in Figure 5, the intergenic sequences of pIP1714 delimited by *vatC* and *repB* also exhibited significant similarities with pUB110.

Example 6: *Plasmid DNA isolation from PIIA^R staphylococci*

10 The staphylococci were grown after overnight incubation at 37°C in 200 ml BHI containing 10 µg/ml of PIIA. After 15 min centrifugation at 8000 rpm, the pellet was resuspended in 25 ml TES (Tris 50 mM, EDTA 1 mM, saccharose 7%). After adding 150 µg of lysostaphin, the mixture was incubated 30 min at 37°C. Then, 2ml of SDS 20% and 6 ml of EDTA 0.25 M were added and the suspension was incubated 15 min at 15 37°C. 8 ml of NaCl 5M were added and the mixture was kept 90 min at +4°C. After 30 min centrifugation at 8000 rpm, the supernatant was incubated 15 min at 37°C with 5 µg of Rnase (Boehringer). 10 µg of Proteinase K were added and the suspension was incubated 15 min at 65°C. DNA was precipitated using isopropanol (0.6 V for 1 V of DNA solution). After 30 min centrifugation at 8000 g, the pellet was washed with 10 ml 20 ethanol 70%. The washed DNA was dried at 56°C, dissolved in 10 ml water and purified by dye-buoyant density centrifugation (ethidium bromide - cesium chloride). The extrachromosomal band was collected. After removing ethidium bromide, the solution of plasmid DNA was dialysed using TE buffer (Tris, 10 mM, EDTA 1 mM, pH 7).

25 **Example 7:** *Plasmid DNA isolation from E. coli*

Cf. QIAfilter plasmid maxi protocol for large-scale preparations and QIAprep Spin plasmid kit protocol for mini-preparations.

Quiagen GmbH and Quiagen Inc. (Hilden, Germany)

	- Plasmid maxi kit	Ref	:	12262
5	- Miniprep kit	Ref	:	27104

Example 8: *Transformation by electroporation of the S. aureus recipient strain, RN4220*

10 1 - Preparation of cells

200ml of BHI was inoculated with 20ml of an overnight culture of RN4220 (*Kreiswirth et al., Nature 1983, 306:709-712*) and incubated at 37°C with shaking. When the OD reached 0.4 at 600 nm, the suspension was kept in ice. The pellet was washed three times with 20 ml of cold Hepes buffer (saccharose 9.31 % - Hepes 0.19 %
15 - pH. 7.4). The pellet was resuspended in 2.5 ml of Hepes buffer containing 10% glycerol. Aliquots of 100 µl cell suspension ($3 \cdot 10^{10}$ /ml) were stored at -80°C.

2 - Electroporation

After thawing at room temperature, the 100 µl aliquot of cells was kept in ice. After
20 adding 10 µl of a solution containing 1 µg of plasmid DNA, the mixture was transferred to a cold 0.2 cm electroporation cuvette. The Gene Pulser (BioRad) was set at 25 uF and 2.5 KV and the Pulse Controller to 100Ω. This produced a pulse with a constant time of 2.3 to 2.5 m sec. The cuvette was removed from the chamber and 1 ml of SOC (2% bactotryptone, 0.5% bacto yeast extract, 10mM NaCl, 2.5mMKCl, 10mM MgCl₂, 10mM
25 MgSO₄, 20 mM glucose) was added. The cell suspension was transferred in a propylene tube and incubated with shaking at 37°C for 1 hr. The suspension was then plated on selective medium, which consisted of BHIA containing 10 µg/ml erythromycin or 10

µg/ml of PIIA. The plates were incubated 48 h at 37°C and the transformants isolated on selective medium. The further studies were carried out on a single isolated colony.

Example 9: Polymerase chain reaction

- 5 DNA was amplified by PCR in a Crocodile II thermal cycler (Appligène) with approximately 10ng of cellular DNA or 1ng of plasmid DNA. The reaction mixture contained 0.6 µM of each oligonucleotide serving as primer, 200 µM of each deoxynucleotide triphosphate, 2.5 U of *Taq* DNA Polymerase (Amersham, Int.), and 1 x buffer (Amersham, Int.). The final reaction volume was adjusted to 100 µl with H₂O
- 10 and the sample was then covered by 50 µl of heavy white mineral oil (Sigma Chemical Co, St. Louis, Missouri).

PCR experiments were carried out at high or low stringency, depending on the primers used. At high stringency, the PCR was performed with a precycle of 3 min at 95°C and 2 min at 60°C, 30 cycles of 20 sec at 72°C, 20 sec at 95°C, 20 sec at 60°C

15 followed by a cycle of 1 min at 72°C. At low stringency, the PCR was performed with a precycle of 5 min at 95°C, 35 cycles of 2 min at 40°C, 1 min 30 sec at 72°C, 30 sec at 95°C followed by a cycle of 4 min at 40°C and 12 min at 72°C. The oligonucleotides used at high stringency are indicated in the Table below.

	PRIMER
<i>vgaB</i>	<p>Oligo I 5'-AAG<u>TCGACT</u>GACAATATGAGTGGTGG-3' <i>SalI</i></p> <p>Oligo II 5'-<u>CTGCAG</u>ATGCCTCAACAGCATCGATATCC-3' <i>PstI</i></p>
<i>vatC</i>	<p>Oligo III 5'- ATGAATTCGCAAATCAGCAAGG -3' <i>EcoRI</i></p> <p>Oligo IV 5'- TCGTCTC<u>GAGCTCT</u>AGGTCC -3' <i>SacI</i></p>
<i>vgbB</i>	<p>Oligo V 5'- CAGCAGTCTAGATCAGAGTGG -3' <i>XbaI</i></p> <p>Oligo VI 5'- CATACGGATCCACCTTTTCC -3' <i>BamHI</i></p>

Example 10: *Labelling of DNA probes*

Plasmid DNA was labelled with [α -³²P]dCTP (110 Tbq mmol⁻¹) by the random printing technique using the Megaprime DNA labelling system (Amersham).

5

Example 11: *Blotting and hybridization*

Hybond-N+membranes (Amersham) were used for blotting. DNA was transferred from agarose gels to the membranes by the capillary blotting method of Southern Blotting. DNA was denatured and fixed to the membranes according to the protocol described in the handbook user of Hybond-N+ membranes.

10

Prehybridization and hybridization were done at 68°C in a mixture containing 5X SSPE (1X SSPE is 0.3 M NaCl, 30 mM tri-sodium citrate), 5X Denhardt's solution, 0.5% (w/v) SDS, and 100 µg ml⁻¹ salmon sperm DNA. The membranes containing DNA transferred from agarose gels were treated with 10 ng ml⁻¹ radiolabeled DNA probe.

- 5 Washing was started with two successive immersions in 2X SSPE, 0.1% SDS, at room temperature for 10 min, followed by one immersion in 1X SSPE, 0.1% SDS, at 68°C for 15 min, and finally by one immersion in 0.1 X SSPE, 0.1% SDS, at 68°C for 15 min. The washed blots treated with the radiolabeled probe were exposed to Fuji RX film at -70°C.

10 **Example 12:** *Nucleotides sequence determination*

- For *vatC* and *vgbB*, the sequencing reaction was performed by PCR amplification in a final volume of 20 µl using 500 ng of plasmid DNA, 5-10 pmoles of primer and 9.5 µl of DyeTerminators premix according to Applied Biosystems protocol. After heating to 94°C for 2 min, the reaction was cycled as the following: 25 cycles of 30s at 94°C, 30s at 55°C, and 4 min at 60°C (9600 thermal cycler Perkin Elmer). Removal of excess of DyeTerminators were performed using Quick Spin columns (Boehringer Mannheim). The samples were dried in a vacuum centrifuge and dissolved with 4µl of deionized formamide EDTA pH 8.0 (5/1). The samples were loaded onto an Applied Biosystems 373A sequencer and run for 12 h on a 4.5% denaturing acrylamide gel.
- 15

- Primers used for sequencing the following genes:

◦ *vatC*

5'-GAAATGGTTGGGAGAAGCATACC-3'	5'-CAGCAATCGCGCCCGTTTG-3'
5'-AATCGGCAGAATTACAAACG-3'	5'-CGTTCCCAATTTCCGTGTTACC-3'

◦ *vghB*

5'-GTTTCTATGCTGATCTGAATC-3'	5'-GTCGTTTGTAATTCTGCCGATT-3'
5'-GGTCTAAATGGCGATATATGG-3'	5'-TTCGAATTCTTTATCCTACC-3'

5

For *vgaB*. DNA was sequenced according to the instructions provided by the T7SequencingTm kit from Pharmacia Biotech (Uppsala, Sweden), procedures C and D.

- Primers used for sequencing the following genes:

◦ *vgaB*

5'-GCTTGGCAAAAGCAACC-3'	5'-TGAATATAGGATAG-3'
5'-TTGGATCAGGGCC-3'	5'-CAATTAGAAGAACCAC-3'
5'-CAATTGTTCACTAGG-3'	5'-GAATTCATTCTATGG-3'
5'-TACACCATTTGTTACC-3'	5'-CAAGGAATGATTAAGCC-3'
5'-GATTCAGATGTTCCC-3'	5'-TCATGGTCGCAATG-3'
5'-GTTGCTTTCGTAGAAGC-3'	5'-GTTATGTCATCCTC-3'
5'-GGTTCATCTACGAGC-3'	5'-GGATATCGATGCTG-3'
5'-GCCAACTCCATTC-3'	5'-CCTAGCTGAACAATTG-3'
5'-GAAGGTGCCTGATCC-3'	5'-ATACTAGAAATGC-3'

Example 13: DNA cloning

A standard protocol was followed for cloning into the vector pOX7, also named
 5 pOX300, the 2.4 kb *Hind*III-*Hae*III fragment of pIP1633 carrying *vgaB* (Fig. 1) and the
 plasmid pIP1714 carrying *vatC* and *vgaB* (Fig. 4), linearized by cleavage with *Hind*III.
 The vector DNA (10-20 µg) and the plasmids used in cloning experiments were cleaved
 with the appropriate restriction enzymes (30 Units) and purified by GeneClean Kit (Bio
 101, La Jolla, Calif.). To avoid religation, the vector cleaved with a single enzyme was
 10 dephosphorylated by 30 min incubation at 37°C with 5 Units of alkaline phosphatase.
 Ligation was carried out in a total reaction volume of 10 µl containing 0.1 µg of the
 vector, 0.1 µg of the plasmid, 0.5 mM ATP, 1 X T4 DNA ligase buffer and 0.1 Weiss
 Unit of T4 DNA ligase. After overnight incubation at 16°C, 1 to 2 µl of the ligation
 mixture are used for transforming competent *E. coli* and the transformants were selected
 15 on solid media containing 100 µg/ml of ampicillin.

Example 14: *Susceptibility to antimicrobial agents*

Susceptibility to antimicrobial agents was determined with a disk diffusion assay and commercially available disks (Diagnostic Pasteur). Additional disks prepared in our laboratory contained streptogramin A (20 µg) or streptogramin B (40 µg).

- 5 - NCCLS: Performance standards for antimicrobial disk susceptibility test, 1984, Approved standard M2-A3, 4:369-402.
- ECCLS: Standard for antimicrobial susceptibility testing by diffusion methods, 1985, ECCLS Document, 5:4-14.

10 Minimal inhibitory concentrations (MICs) of antibiotics were determined by serial twofold dilutions of antibiotics in MHA (Ericson H.M. and S.C. Sherris, ActaPathol. Microbiol. Scand., 1971, Suppl. 217:Section B).

 Despite the relatively low frequency of detection of SgA^R staphylococci (1-10%) (Loncle et al., 1993; Allignet et al., 1996), four genes encoding resistance to streptogramin A have been detected and other resistance gene(s) are suspected to be

15 carried by staphylococci. Surprisingly, the present and previous studies (Allignet et al., 1996) indicate that staphylococcal plasmids carrying two genes encoding streptogramin A resistance by two distinct mechanisms (inactivation by acetyltransferases and increased efflux) are widespread among staphylococci (32 of the 48 plasmids investigated).

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WHAT IS CLAIMED IS:

1. A purified polynucleotide comprising the nucleotide sequence selected from the group consisting of SEQ ID NO: 1 or a fragment derived from SEQ ID NO: 1 containing 15 to 40 nucleotides, SEQ ID NO: 11, and SEQ ID NO: 12.
2. A purified peptide comprising the amino acid sequence encoded by the nucleotide sequence selected from the group consisting of SEQ ID NO: 1 or a fragment derived from SEQ ID NO: 1 containing 15 to 40 nucleotides, SEQ ID NO: 11, and SEQ ID NO: 12.
- 10 3. A purified peptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 4 or a fragment derived from SEQ ID NO: 4 containing at least 10 amino acids, SEQ ID NO: 7, and SEQ ID NO: 8.
4. A purified polynucleotide comprising the nucleotide sequence of SEQ ID NO: 3 or a fragment derived from SEQ ID NO: 3 containing 15 to 40 nucleotides.
- 15 5. A purified peptide comprising the amino acid sequence encoded by the nucleotide sequence selected of SEQ ID NO: 3 or a fragment derived from SEQ ID NO: 3 containing 15 to 40 nucleotides.
6. A purified peptide comprising the amino acid sequence of SEQ ID NO: 6 or a fragment derived from SEQ ID NO: 6 containing at least 10 amino acids.
- 20 7. A purified polynucleotide comprising the nucleotide sequence selected from the group consisting of SEQ ID NO: 2 or a fragment derived from SEQ ID NO: 2 containing 15 to 40 nucleotides, SEQ ID NO: 13, and SEQ ID NO: 14.
8. A purified peptide comprising the amino acid sequence encoded by the nucleotide sequence selected from the group consisting of SEQ ID NO: 2 or a fragment derived from SEQ ID NO: 2 containing 15 to 40 nucleotides, SEQ ID NO: 13, and SEQ ID NO: 14.
- 25

9. A purified peptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 5 or a fragment derived from SEQ ID NO: 6 containing at least 10 amino acids, SEQ ID NO: 9, and SEQ ID NO: 10.

10. A composition of polynucleotide sequences useful for the detection of resistance to streptogramins A and/or B and related compounds comprising at least a nucleotide sequence selected from the group consisting of the polynucleotide or gene or cDNA *pvgaB*, *vgbB*, and *vatC*.

11. A composition of polynucleotide sequences useful for the detection of resistance to streptogramin A or streptogramin B and related compounds comprising at least an amino acid sequence from a polypeptide encoded by a polynucleotide selected from the group consisting of the polynucleotide, gene, or cDNA *vgaB*, *vgbB*, and *vatC*.

12. A composition of polynucleotide sequences encoding resistance to streptogramins and related compounds, or inducing streptogramin resistance in Gram-positive bacteria, wherein said composition comprises at least a nucleotide sequence encoding a molecule containing ATP binding motifs conferring resistance to streptogramin A and related compounds and at least a nucleotide sequence selected from the following sequences:

- a) a nucleotide sequence encoding an acetyltransferase conferring resistance to streptogramin A and related compounds; and
- b) a nucleotide sequence encoding a lactonase conferring resistance to streptogramin B and related compounds.

13. A composition of polynucleotide sequences encoding resistance to streptogramins and related compounds, or inducing streptogramin resistance in Gram-positive bacteria, wherein said composition comprises at least a nucleotide sequence encoding an acetyltransferase conferring resistance to streptogramin A and related compounds and at least a nucleotide sequence selected from the following sequences:

- a) a nucleotide sequence encoding a molecule containing ATP binding motifs conferring resistance to streptogramin A and related compounds; and
- b) a nucleotide sequence encoding a lactonase conferring resistance to streptogramin B and related compounds.

5 14. A composition of polynucleotide sequences encoding resistance to streptogramins and related compounds, or inducing streptogramin resistance in particular in Gram-positive bacteria, wherein said composition comprises at least a nucleotide sequence encoding a lactonase conferring resistance to streptogramin B and related compounds and at least a nucleotide sequence selected from the following sequences:

- 10 a) a nucleotide sequence encoding a material containing ATP binding motifs conferring resistance to streptogramin A and related compounds; and
- b) a nucleotide sequence encoding an acetyltransferase conferring resistance to streptogramin A and related compounds.

15 15. A composition of polynucleotide sequences according to any one of the claims 12 to 14, wherein the polynucleotide sequence encoding a molecule containing ATP binding motifs confers resistance to streptogramin A and related compounds in *Staphylococcus*, and wherein the polynucleotide corresponds to a *vgaB* nucleotide sequence represented in the SEQ ID NO: 1 or to a nucleotide sequence having at least

20 70 % of identity with the *vgaB* complete nucleotide sequence, or corresponds to a polynucleotide hybridizing with said SEQ ID NO: 1 under stringent conditions, or to a fragment containing between 20 and 30 nucleotides of SEQ ID NO: 11 or SEQ ID NO: 12 or, wherein the polynucleotide sequence encodes a polypeptide having at least 60 % homology with the complete SEQ ID NO: 4 or 80 % with SEQ ID NO: 11 or SEQ ID

25 NO: 12.

16. A composition of claim 15, wherein the polynucleotide sequence encoding a molecule containing ATP binding motifs confers resistance to streptogramin A and related compounds in *Staphylococcus aureus*.

17. A composition of polynucleotide sequences according to any one of the claims 12 to 14, wherein the polynucleotide sequence encoding an acetyltransferase confers resistance to streptogramin A and related compounds in *Staphylococcus*, and wherein the polynucleotide corresponds to a *varC* nucleotide sequence represented in the
5 SEQ ID NO: 2 or to a nucleotide sequence having at least 70 % of identity with the *varC* complete nucleotide sequence, or corresponds to a polynucleotide hybridizing with said SEQ ID NO: 2 under stringent conditions or to a fragment of SEQ ID NO: 2 containing between 20 and 30 nucleotides, or to SEQ ID NO: 13 or SEQ ID NO: 14, or wherein the polynucleotide sequence encodes a polypeptide having at least 60 % homology with the
10 complete SEQ ID NO: 5 or 80 % with SEQ ID NO: 13 or SEQ ID NO: 14.

18. A composition of claim 17, wherein the polynucleotide sequence encoding an acetyltransferase confers resistance to streptogramin A and related compounds in *Staphylococcus cohnii*.

19. A composition of polynucleotide sequences according to any one of the
15 claims 12 to 14, wherein the polynucleotide sequence encoding a lactonase confers resistance to streptogramin B and related compounds in *Staphylococcus*, and wherein the polypeptide corresponds to a *vgbB* nucleotide sequence represented in the SEQ ID NO: 3 or to a nucleotide sequence having at least 70 % of identity with the *vgbB* complete nucleotide sequence, or corresponds to a polynucleotide hybridizing with said SEQ ID
20 NO: 3 under stringent conditions or to a fragment of said SEQ ID NO: 3 containing 20 to 40 nucleotides, or wherein the polynucleotide sequence encodes a polypeptide having at least 60 % homology with the complete SEQ ID NO: 6.

20. A composition of claim 19, wherein the polynucleotide sequence encoding a lactonase confers resistance to streptogramin A and related compounds in
25 *Staphylococcus cohnii*.

21. A composition of polynucleotide sequences according to claim 12 or 13, wherein said composition comprises at least one nucleotide sequence encoding a molecule containing ATP binding motifs conferring resistance to streptogramin A and related

compounds and at least one nucleotide sequence encoding an acetyltransferase conferring resistance to streptogramin A and related compounds.

22. A composition of polynucleotide sequences according to claim 21, wherein said composition comprises at least a *vgaB* nucleotide sequence encoding a molecule containing ATP binding motifs conferring resistance to streptogramin A and related compounds and at least a *varB* nucleotide sequence encoding an acetyltransferase conferring resistance to streptogramin A and related compounds.

23. A purified polynucleotide that hybridizes specifically under stringent conditions with a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14.

24. A polynucleotide fragment comprising at least 10 nucleotides, that hybridizes under stringent conditions with a sequence according to any one of claims 1-9 or 23 or the polynucleotide complementary fragment thereof.

25. A polynucleotide fragment of claim 12, wherein said fragment corresponds to at least one of the following sequences:

- Oligo I 5'-AAGTCGACTGACAATATGAGTGGTGG-3'
- Oligo II 5'-CTGCAGATGCCTCAACAGCATCGATATCC-3'.

26. A polynucleotide fragment of claim 12, wherein said fragment corresponds to at least one of the following sequences:

- Oligo III 5'- ATGAATTCGCAAATCAGCAAGG -3'
- Oligo IV 5'- TCGTCTCGAGCTCTAGGTCC -3'.

27. A polynucleotide fragment of claim 12, wherein said fragment corresponds to at least one of the following sequences:

- Oligo V 5'- CAGCAGTCTAGATCAGAGTGG -3'
- Oligo VI 5'- CATACGGATCCACCTTTTCC -3'.

28. A recombinant DNA sequence comprising at least a nucleotide sequence according to any one of claims 1, 4, or 7 under the control of regulatory elements that

regulate the expression of resistance to antibiotics of the streptogramin family in a defined host.

29. A recombinant vector comprising the DNA sequence of claim 31, wherein the vector comprises a plasmid pIP1633 deposited with the C.N.C.M. under the Accession
5 No. I-1768 or a plasmid pIP1714 deposited with the C.N.C.M. under the number I-1877 on June 18, 1997.

30. A recombinant cell host comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 3, SEQ ID NO: 2, SEQ ID NO: 13, and SEQ ID NO: 14, or the recombinant vector of
10 claim 32.

31. A purified polypeptide or a peptide fragment having at least 10 amino acids, which is recognized by antibodies directed against a polynucleotide sequence conferring resistance to streptogramin and related compounds, corresponding to a polynucleotide sequence according to any one of claims 1, 4, or 7.

32. A polynucleotide comprising the full length coding sequence of a
15 *Staphylococcus* streptogramin A and/or B resistant gene containing a polynucleotide sequence according to any one of claims 1, 4, or 7.

33. A monoclonal or polyclonal antibody directed against a polypeptide or a peptide fragment encoded by the polynucleotide sequences according to any one of claims
20 1, 4, or 7.

34. A method of detecting the presence of bacterium harboring the polynucleotide sequences according to any one of claims 1, 4, or 7 in a biological sample comprising:

25 a) contacting bacterial DNA of the biological sample with a primer or a probe according to any one of claims 24-27, which hybridizes with a nucleotide sequence encoding resistance to streptogramins;

- b) amplifying the nucleotide sequence using said primer or said probe; and
- c) detecting the hybridized complex formed between said primer or probe with the DNA.

5 35. A kit for detecting the presence of bacterium having resistance to streptogramin A and/or streptogramin B and harboring the polynucleotide sequences according to any one of the claims 1, 4, or 7 in a biological sample, said kit comprising:

- a) a polynucleotide probe according to any one of claims 24-27; and
- 10 b) reagents necessary to perform a nucleic acid hybridization reaction.

36. A kit for detecting the presence of bacterium having resistance to streptogramin A and harboring the polynucleotide sequences according to claim 1 or claim 7 in a biological sample, said kit comprising:

- 15 a) a polynucleotide probe according to claim 24-26; and
- b) reagents necessary to perform a nucleic acid hybridization reaction.

37. A method of screening active antibiotics for the treatment of the infections due to Gram-positive bacteria, comprising the steps of:

- 20 a) bringing into contact a Gram-positive bacteria having a resistance to streptogramin A or streptogramin B and related compounds and containing the polynucleotide sequences according to any one of the claims 1, 4, or 7 with the antibiotic; and
- b) measuring an activity of the antibiotic on the bacteria having
- 25 a resistance to streptogramins and related compounds.

38. A method of screening for active synthetic molecules capable of penetrating into a bacteria of the family of staphylococci, wherein the inhibiting activity of these

molecules is tested on at least a polypeptide encoded by the polynucleotide sequences according to any one of claims 1, 4, or 7 comprising the steps of:

- a) contacting a sample of said active molecules with the bacteria;
- 5 b) testing the capacity of the active molecules to penetrate into the bacteria and the capacity of inhibiting a bacterial culture at various concentration of the molecules; and
- c) choosing the active molecule that provides an inhibitory effect of at least 80% on the bacterial culture compared to an untreated culture.

10

39. An *in vitro* method of screening for active molecules capable of inhibiting a polypeptide encoded by the polynucleotide sequences according to any one of claims 1, 4, or 7, wherein the inhibiting activity of these molecules is tested on at least said polypeptide, said method comprising the steps of:

- 15 a) extracting a purified polypeptide according to claim 31;
- b) contacting the active molecules with said purified polypeptide;
- c) testing the capacity of the active molecules, at various concentrations, to inhibit the activity of the purified polypeptide; and
- 20 d) choosing the active molecule that provides an inhibitory effect of at least 80 % on the activity of the said purified polypeptide.

40. A composition of a polynucleotide sequence encoding resistance to streptogramins and related compounds, or inducing resistance in Gram-positive bacteria, wherein said composition comprises a nucleotide sequence corresponding to the resistance phenotype of the plasmid pIP1633 deposited with the C.N.C.M. under the
25 Accession No. I-1768 and of the plasmid pIP1680 deposited with the C.N.C.M. under the Accession No. I-1767 and of the plasmid pIP1714 deposited with the C.N.C.M. under the number I-1877 on June 18, 1997.



41. A method of detecting the presence of bacterium harboring the polynucleotide sequences according to claim 1 or claim 7 in a biological sample, said method comprising the steps of:

- 5 a) contacting said sample with an antibody according to claim 36 that recognizes a polypeptide encoded by said polynucleotide sequences; and
- b) detecting said complex.

42. A diagnostic kit for *in vitro* detecting the presence of bacterium harboring the polynucleotide sequences according to claim 1 or claim 7 in a biological sample, said kit
10 comprising:

- a) a predetermined quantity of monoclonal or polyclonal antibodies according to claim 33;
- b) reagents necessary to perform an immunological reaction between the antibodies and a polypeptide encoded by said polynucleotide
15 sequences; and
- c) reagents necessary for detecting said complex between the antibodies and the polypeptide encoded by said polynucleotide sequences.

INTERNATIONAL SEARCH REPORT

Intr. 'tional Application No

PCT/IB 98/00962

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/54 C12N9/10 C12N15/31 C07K14/31 C12N15/55
C12N9/18 C12N15/74 C12N1/21 C12Q1/14 C12Q1/34
C12Q1/48 C12Q1/68 G01N33/569 C07K16/12 C07K16/40

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ALLIGNET J. ET AL.: "Sequence of a staphylococcal plasmid gene, vga, encoding a putative ATP-binding protein involved in resistance to virginiamycin A-like antibiotics" GENE, vol. 117, 1992, pages 45-51, XP002083993 cited in the application see the whole document	1-3, 12-16, 23,24, 28, 31-33, 37-42
Y		21,22
A		34-36

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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

17 November 1998

Date of mailing of the international search report

01.03.99

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2

Authorized officer

PC1/IB 98/00962

IPC 6 // (C12N1/21, 1:19, 1:445)

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ALLIGNET J. ET AL.: "Sequence of a staphylococcal gene, vat, encoding an acetyltransferase inactivating the A-type compounds of virginiamycin-like antibiotics"	21,29, 34-36,40
Y	GENE, vol. 130, 1993, pages 91-98, XP002083994 cited in the application see page 92, left-hand column, paragraph 1 see page 93; figure 2 --- -/--	21

☒

Further documents are listed in the continuation of box C.

☒

Patent family members are listed in annex.

^o Special categories of cited documents :

P document published prior to the international filing date but later than the priority date claimed

***&** document member of the same patent family

Date of the actual completion of the international search

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Date of mailing of the international search report

Name and mailing address of the ISA

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NL - 2280 HV Rijswijk

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INTERNATIONAL SEARCH REPORT

International Application No

PC1/IB 98/00962

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>ALLIGNET J. AND EL SOLH N.: "Diversity among the Gram-positive acetyltransferases inactivating Streptogramin A and structurally related compounds and characterization of a new staphylococcal determinant, vatB"</p> <p>ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, vol. 39, no. 9, September 1995, pages 2027-2036, XP002084725</p> <p>cited in the application</p>	29,40
Y	<p>see page 2027</p> <p>see page 2029, right-hand column, paragraph 5</p>	22
X	<p>---</p> <p>WO 96 08582 A (BERGERON MICHEL G.; OUELLETTE MARC; ROY PAUL H. (CA))</p> <p>21 March 1996</p> <p>see abstract</p> <p>see page 17, line 6-32</p> <p>see page 38; table 8</p> <p>Seq.ID:176</p> <p>see page 151 - page 152</p> <p>---</p>	<p>1,2,</p> <p>12-16,</p> <p>21,23,</p> <p>24,32,</p> <p>34-36</p>
P,X	<p>ALLIGNET J. AND EL SOLH N.:</p> <p>"Characterization of a new staphylococcal gene, vgaB, encoding a putative ABC transporter conferring resistance to streptogramin A and related compounds"</p> <p>GENE,</p> <p>vol. 202, no. 1/2, 20 November 1997, pages 133-138, XP002083995</p> <p>see the whole document</p> <p>-----</p>	<p>1-3,</p> <p>10-16,</p> <p>21-25,</p> <p>28-32,</p> <p>34-36,40</p>

INTERNATIONAL SEARCH REPORT

national application No.

PCT/IB 98/00962

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

See Further Information sheet enclosed.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-3, 15, 16, 25 all totally; 10-14, 21-24, 28-42 all partially.

Polynucleotide comprising the nucleotide sequence as in Seq.ID:1, fragments, hybridizing sequences and complementary sequences thereof. Corresponding polypeptide comprising the aminoacid sequence as in Seq.ID:4 or fragments thereof. Recombinant vector comprising said DNA sequence, recombinant host cell comprising said polynucleotide. Antibody directed against said polypeptide. Application of said polynucleotide or of said antibody in diagnostics, kits thereof. Methods of screening involving bacteria containing said polynucleotide, or said polypeptide.

2. Claims: 4-6, 19, 20, 27 all totally; 9-14, 23, 24, 28-35, 37-40 all partially.

Idem as invention 1 but concerning Seq.ID:3 and Seq.ID:6.

3. Claims: 7, 8, 17, 18, 26 all totally; 9-14, 21-24, 28-42 all partially.

Idem as invention 1 but concerning Seq.ID:2 and Seq.ID:5.

INTERNATIONAL SEARCH REPORT

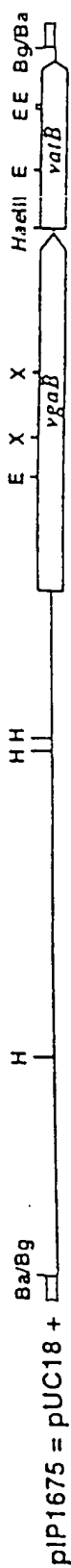
Information on patent family members

International Application No

PCT/IB 98/00962

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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Figure 1A



pip1717 = pOX300 +

Figure 1B



1000 bp

Exo RI

Figure 2

Q L E Q A I K L K X N K A Q G H I K P P S K T M G T S E S R I H K M Q H A T K Q
 caattggagcaagctataaagctaaagagaataangggcgaaggaatgattaaagcccccctcaaaaacaaatgggaacatctgaatctctagaatattggaaaatgcaacatgctactaaacaa 1440
 K K H H R N T K S L E T R I D K L N H V E K I K E L P S I K M D L P N R E Q P H
 aaaaagatgcatagaatacgaatcgttggaaacgaaatagataaattaaatcatgtagaaaaataaaaagagcttccctctattcaaaatggattacctaantagagagcaattccat 1560
 G R N V I S L K N L S I K P N N Q P L W R D A S P V I K C O E X V A I I Q H N H O
 ggtcgcaatgtaattagtttaaaaaacttatctataaaaatttaataatcaantttctttggagagatgcttcatattgctattaaaggtggagaaaaaggttgcataantggtaacaatgggt 1680
V Q X T T L L K L I L E K V E S V I I S P S V K I C Y V S Q N L D V L Q S H K S
 gtggaaaaaacacacattgttgagctgattctagaaaagtagaaatcgatgaatcgaatgaatcaccatcagttcaaaatggatcagtcacgtcnaaaactttagtcttacaatctcataaatct 1800
 I L E N V M S T S I Q D E T I A R I V L A R L H P Y R M D V H K E I M V L S G G
 atcttagaaaaatgttcaatgtctacctccattcnaagatgaanccaatagcaagaattgttcttagcaagattacantttttatcgcaantgatgttcataanaagaaataaattgttttgagtggtgga 1920
 E Q I K V A F A K L P V S D C N T L I L D E P T H Y L D I D A V E A L E B L L I
 gaacaaataaagggttgcgttttggcgaagctatttggtagcgattgtaatacatttaantttcttgatgaanccaanccaactatttggatctcgatgctgttggcgcatctogaagaattgttaatt 2040
 T Y E G V V L P A S H D K K P I Q N L A B Q L L I I E H M K V K K P E Q T Y I E
 acctatgaagggtgttgttatttgcgttcccatgntaaaantttatacaaaaacctagctgaacaattgttaataatagaanaataaagtgaaaaaattcgaaggaaacatatatagaa 2160
 Y L K I K D K P K L N T N E K E L K E K H I L E H Q I S S L L S K I S M E E N
 tatttaaaaattaaagataaaacaaattaaatacaaaatgaabaaagaaactcaaaagaaanaaagatgatactagaatgcaaaatttcatctattattangtaaaaatctcaatggagaaaaat 2280
 E E K N K E L D E K Y K L K L K B L K S L H K H I
 gaagaaaaaaacaaagaattagatgaagaagtaacaaattgaattaaagaattgaabaaagctaaataaaaatattttttonnaataaaattatatattaataggagggttttaaaaatgaaatagggc 2400
 Surtw/B Harll
 EodryaB
 P D P N
 ctgatccaaat 2411

Figure 2 (cont.)

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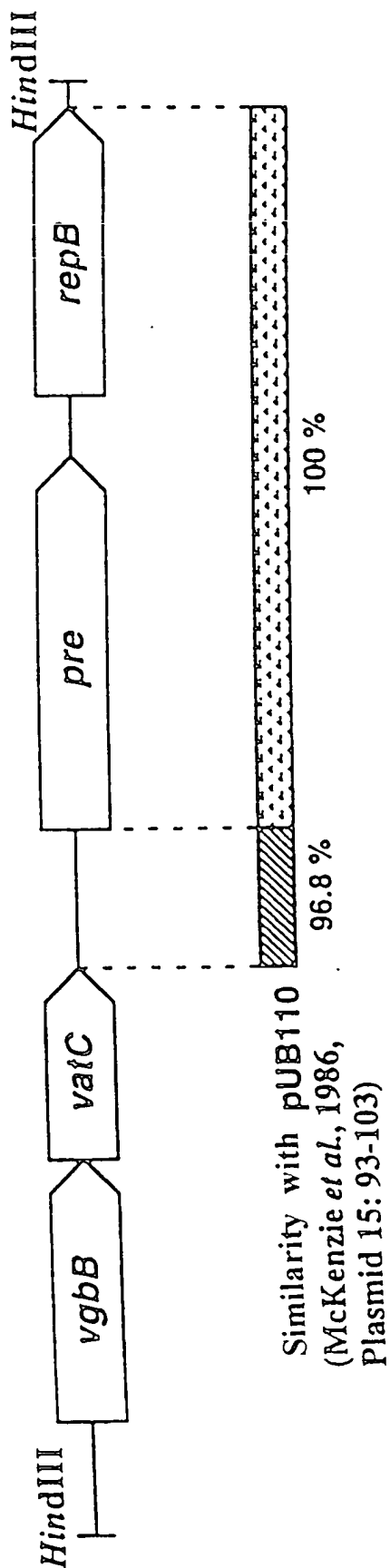
Figure 3

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VgaB	SIKFNNQFLWRDASFVIKGEKVAIIIGNNGVGKTTLLKLLILEKVESVIIISPSVKIGYVSQ	357
Vga	SGTIEGRVLWKAJSFIRGGDKMAIIGSNGTGKTFIKKIVHGNPGISLSPSVKIGYFSQ	338
	WA	
VgaB	NLDVLQSHKSILENVVMTSIQDETIARIVLARLHFYRNDVHKEINVLSGGEQIKVAFKL	417
Vga	KIDTLELDKSILENVQSSSQNETLIRTLARMHFFRDDVYKPISVLSGGERVKVALTKV	398
	loop 3'	
VgaB	FVSDCNTLILDEPTNYLDIDAVEALEELLITYEGVLFASHDKKFIQNLAEQLLIENNK	477
Vga	FLSEVNTLVLDPTNFDMEAI EAFESLLKEYNGSIIFVSHDRKFIKVA TRIMTIDNKE	458
VgaB	VKKFEGTYIEYLKIKDKPKLNTNEKELKEKMMILEMQISSLLSKISMEENEKKNKELDEK	537
Vga	IKIFDGTY-EQFKQAEKPTRNIKE----DKLLLETKITEVLSRLSIEPSEE----LEQE	509
VgaB	YKLLKELKSLNFGNI	552
Vga	FQNLINERKRNLDK--	522
	WB	

Figure 3 (cont.)

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1 kb

Figure 4

Start rbb
 RBS ° M N P Y L E E P N L S I P D S G P Y G I T S S E D G K
 aggagtttttcggttcaaaaataattggagggaatgtttaaactgtctatcccgattcagggtccatcaggtataaacttcacagaaacggaag
 V W F T Q H K A N K I S S L D Q S G R I K E P E V P T P D A K V M C L I V S S L
 tatggttcacacacataaggcaacaaacacgacgtctagatcagagtggttaggataaaaadaficgaagttccctacccctgatgctaaagtgtgtttaattgtatcttcaattg
 XbaI
 EcoRI
 G D I W P T E B N G A N K I G K L S K K G G P T E Y P L P Q P D S G P Y G I T E G
 gagacatatgtttacagagaaatgggtgcanaataaatacgaagctctcaaaaaaagggtggttttacagaataatccattgccacagccggattcttggtcccttacggaataacggaaggtc
 L N G D I W P T Q L N G D R I G K L T A D G T I Y E Y D L P N K G S Y P A P I T
 taaatggcgatataatgtttaccacaaattgaatggagatcgtataggaaaagttgacagctgattgggactatttatgaataatgattttgccaataaagggtatcttaccctgctttttattactt
 L G S D N A L W P T B N Q N N S I G R I T N T G K L E E Y P L P T N A A A P V G
 taggttcggataacgcactttggttcacggagaaacaaataattctatttggaaggattacaataacagggaaaattagaagaataatcctctaccacaacaaatgcagcggctccagtggtgta
 I T S G N D G A L W P V E I M G N K I G R I T T G E E I S E Y D I P T P N A R P
 tcactagtgttaacgagtggtgcactctgtttgtcgaaaattatgggcaacaaataggctgaatcactacaactgggtgagatttagcgaataatgatattccaaactccaaacgcacgtccac
 H A I T A G K N S E I W P T E W G A N Q I G R I T N D K T I Q E Y Q L Q T E N A
 acgctataaccggggaataatagcgaataatggttttactgaatgggggcaacaaatcgaatcggcagaattacaaaacgacaaaacaaattcgaataatcaacttcaaacagaaaaatgcgg
 End rbb
 End rbs
 RBS ° M K W Q N
 E P H G I T P G K D G S V W P A L K C K I G K L N L N E °
 aacctcatggtatccctttggaaaagatggatccgtatggtttgcattaaaatgttaaaattgggaagctgaattttgaacgaatgagatgggagtgagcaaatatttatgaaatgggcaaaa
 BamHI
 Q Q G P N P E E I Y P I E G N K H V Q P I K P S I T K P N I L V G E Y S Y D S
 tcagcaaggcccaatccagaagaataatataccctatagaaggtaataaacatgtttcaatttataaacacatctatacaaaaagcccaataatttttagttggggaatatattcatattacgataag
 K D G E S P E S Q V L Y H Y E L I G D K L I L G K P C S I G P G T T P I M N G A
 taaagatggtgaatcttttgaaagccaagttctttatcactatgaattgattggggataaaactaatattagggaagttttgttctatttggaccccgaaacgacatttataatgaatggggc
 N H R H D G S T P P N L P G N G W E K H T P T L E D L P Y K G N T E I G N D V
 taatcatcgtatggtgttcaacatttccattcaatcttttcggaaaatggttggggaagcataccctacatttggaagaccttctctataaagggttaacacggaatattgggaacgatgt
 W I G R D V T I M P G V K I G N G A I I A A K S V V T K N V D P Y S V V G G N P
 ttgattggacgagatgtgacaattatgcccggtgttaaaaataggaaaacggggctattattgcagcaaaatcggttgtgacaanaagacgttgatcttattcagttgttggcggtaatcc
 S R L I K I R P S K E K I A A L L K V R W D L E I E T I M E N I D C I L N G D
 ttcacgatttaataagataagggttttccaaaggaaaataatcgacgattactactaaaagtggttgggacctagagatagagacgataaaatgaaaatatgtgattgcatctcctgaatggtga
 End rbc

Figure 5

End rbc
 I K K V K R S °
 tataaaaaagggttaaaaagaagttagaaaaacgaattttgttttaggtta

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PCR Primers

*vatC*Oligo III 5'-atgaattcgcaaatcagcaagg-3'
EcoRIOligo IV 5'-tcgtctcgagctctaggtcc-3'
SacI

Figure 6A

*vgbB*Oligo V 5'-cagcagctctagatcagagtgg-3'
XbaIOligo VI 5'-catacggatccacctttlcc-3'
BamHI

Figure 6B

vga B

Oligo I 5'-AAGTCGACTGACAAATATGAGTGGTGG-3'

Oligo II 5'-CTGCAGATGCCTCAACAGCATCGATATCC-3'

Figure 6C

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SEQ ID NO: 1

Seq *vgaB*

ATGCTTAAAATCGACATGAAGAATGTAAAAAATATTATGCAGATAAATTAATTTTAAATATAAA
AAAGATTTATAGTGGGGATAAAATAGGTATTGTAGGTAAGAATGGAGTTGGCAAAACAACACTTT
TAATAAAAGGACTAATAGAGATTGACGAAGGAAATATAATTATAAGTAAAAAACAACATTATAAA
TCTCAATTAGAAGAACCACATAGTAAGATAATTGATGGAAAATATGCTTCAATATTTCAAGTTGA
GTGGAATGACAATATGAGTGGTGGTGAAAAAAGTAGATTTAACTAGCAGAGGGATTTCAAGATC
CTTTAANTGCTCGTAGATGAACCTACAAGTAATTTAGATATCGAAGGAATAGAGTTGATAACAAAT
AAAGAGTACCGTGATACTTTTTTGGTAGTATCTCATGATAGAATTTTTTTAGATCAAGTTTGTAC
TTTTGAAATTGAAAATGGATATATTAGAGAATTCATCGGTAATTATACAACTATATAGAGCAAA
TGCTTCTACGAAAGCAACAAGAAGATAAGAAAAGTATAATTCTAAAAGAAAGCAATTGGAGCAA
AAGCTAAAAGAGAATAAGGCGCAAGGAATGATTAAAGCCCTTCAAAAACAATGGGAACATCTGA
AATATGGAAAATGCAACATGCTACTAAACAAAAAAGATGCATAGAAATACGAAATCOTTGGAAA
TAGATAAATTAAATCATGTAGAAAAAATAAAAGAGCTTCCTTCTATTAAATGGATTACCTAAT
CAATTTTCATGGTTCGCAATGTAATTAGTTTAAAAAAGTTATCTATAAAATTTAATAATCAATTTCT
AGATGCTTCATTTGTCATTAAAGGTGGAGAAAAGGTTGCTATAATTGGTAACAATGOTGTAGQAA
CATTGTTGAAGCTGATTCTAGAAAAAGTAGAATCAGTAAATAATATCACCATCAGTTAAAATTGGA
AGTCAAAACTTAGATGTTCTACAATCTCATAAATCTATCTTAGAAAAATGTTATGTCTACCTCCAT
TGAAACAATAGCAAGAATTGTTCTAGCAAGATTACATTTTTATCGCAATGATGTTCTATAAGAAA
TTTTGAGTGGTGGAGAACAAATAAAGGTTGCTTTTGCCAAGCTATTTGTTAGCGATTGTAATACA
CTTGATGAACCAACAACTATTTGGATATCGATGCTGTTGAGGCATTAGAAGAATTGTTAATTAC
AGGTGTTGTGTTATTTGCTTCCCATGATAAAAAATTTATACAAAACCTAGCTGAACAAATTGTTAA
AAAATAATAAAGTGA AAAAATTGGAAGGAACATATATAGAATATTTAAAAATTAAGATAAACCA
AATACAAATGAAAAAGAACTCAAAGAAAAAAGATGATACTAGAAATGCAATTTTCATCATTATT
AATCTCAATGGAAGAAAATGAAGAAAAAACAAGAATTAGATGAAAAGTACAAATTGAAATTAA
TGAAAAGCCTAAATAAAAAATATT

SEQ ID NO: 3

Seq *vgaB*

ATGAATTTTATTTAGAGGAGTTTAACTTGTCTATTCCCGATTGAGGTCCATACGGTATAACTTC
AGACGGAAAGGTATGGTTCACACAACATAAGOCAAAACAAATCAGCAGTCTAGATCAGAGTGGTA
AAGAATTCGAAGTTCCTACCCCTGATGCTAAAGTGATGTGTTTAAATTGTATCTTCACTTGGAGAC
TTTACAGAGAATGGTGCAAATAAAATCGGAAAGCTCTCAAAAAAGGTGGCTTTACAGAATATCC
ACAGCCGGATTCTGGTTCCTTACGGAATAACGGAAGGTCTAAATGGCGATATATGGTTTACCCAAT
GAGATCGTATAGGAAAGTTGACAGCTGATGGGACTATTTATGAATATGATTTGCCAAATAAGGGA
CCTGCTTTTATTACTTTAGGTTTCGGATAACGCACCTTTGGTTTACGGGAGAACC AAAATAATTCTAT
GATTACAAATACAGGGAAATTAGAAGAATATCCTCTACCAACAAATGCAGCGGCTCCAGTGGGTA
GTGGTAACGATGGTGCACCTGCGTTTGTGCAAAATTATGGGCAACAAATAGGTGCAATCACTACA
GAGATTAGCGAATATGATATTCCAATCCAAACGCACGTCCACACGCTATAACCGCGGGGAAAAA
AATATGGTTTACTGAATGGGGGGCAAATCAAATCGGCAGAATTACAAACGACAAAACAATTCAAG
AACTTCAAACAGAAAATGCGGAACCTCATGGTATTACCTTTGGAAAAGATGGATCCGTATGGTTT
AAATGTAAAATTGGGAAGCTGAATTTGAACGAA

Figure 7

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SEQ ID NO: 2

Seq v2tC

ATGAAATGGCAAATCAGCAAGGCCCAATCCAGAAGAAATATACCCTATAGAAGGTAATAAAC
AATTTATTAAACCATCTATAACAAAGCCCAATATTTTAGTTGGGGAATATTCATATTACGATAG
TGGTGAATCTTTTGAAAGCCAAGTTCTTTATCACTATGAATTGATTGGGGATAAACTAATATTA
TTTTGTTCTATTGGACCCGGAACGACATTTATAATGAATGGGGCTAATCATCGTATGGATGGTT
TTCCATTCAATCTTTTCGGAAATGGTTGGGAGAAGCATACCCCTACATTGGAAGACCTTCCTTA
TAACACGGAAATTGGGAACGATGTTTGGATTGGACGAGATGTGACAATTATGCCCGGTGTAAAA
AACGGGGCTATTATTGCAGCAAAATCGGTTGTGACAAAGAACGTTGATCCTTATTCAGTTGTTG
ATCCTTCACGATTAATTAAGATAAGGTTTTCCAAGGAAAAAATCGCAGCATTACTAAAAGTAAG
GGACCTAGAGATAGAGACGATAAATGAAAATATTGATTGCATCCTGAATGGTGATATAAAAAAG
AGAAGT

Figure 7 (cont.)

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SEQ ID NO: 4

VgaB

MLKIDMTKNVKKYYADKLIILNIKELKRIYSGDKIGIVGKNGVGKTTLLKIIK
GLIEIDEGNIIISSEKTTIKYISQLEEPHSKIIDGKYASIFQVENKWNNDNM
SGGEKTRFKLAEGFQDQCSLMLVDEPTSNLDIEGIELITNTFKFYRDTFL
VVSHDRIFLDQVCTKIFEIENGYIRKFIGNYTNYIEQKEMLLRKQQEYE
KYNKSRKQLEQAIKLKENKAQGMIXPPSKTMGTSESRIWKMQHATKQKQM
HRNTKSLSTRIDKLNHVEXIKELPSIKMDLPNREQFHGRNVISLKNLSIK
FNNQFLWRDASPVIKGGEKVAIIGNNGVGKTTLLKLIILEKVESVIISPSV
KIGYVSQNLVDVLQSHKSILENVMSTSIQDETIARIVLARLHFYRNDVHKE
INVLSGGEQIKVAPAKLPVSDCNTLIIDBPTNYLDIDAVEALEELLITYE
GVVLFASHDKKFIQNLAEQLLIENNKVKKFEPTYIHYLKIIDKPKLNTN
EKELKPKQMIEMQISSLLSKISMEENEEKNKELDEKYKLKLKELKSLNK
NI

SEQ ID NO: 6

VgbB

MNFYLEEFNLSIPDSGPYGITSSSEDGKXWFTQHKANKISSLDQSGRIKEF
EVPTPDAKVMCLIVSSIGDIWFTENGANKIGKLSKKGGFTEYPLPQPDG
PGITEGLNGDIWFTQLNGDRIGKLTADGTIYEYDLPNKGSYPAPITLGSB
NALWFTENQNNSIGRITNTGKLEFYPLPTNAAAPVGITSGNDGALWFVEI
MGNKIGRITTTGEISEYDIPTPNARPHAITAGKNSIWFTEWGANQIGRI
TNDKTIQEQLOQTENASPHGITTFGKDGSVWPALKCKIGKLNLE

SEQ ID NO: 5

VatC

MKWQNQQGPNPEEIIYPPEGNKHVQPIKPSITKPNILVGEYSYYDSKDGES
FESQVLYHYELIGDKLILGKFCSIGPGTTFIMNGANHRMDGSTFPFNLF
NGWERHTPTLEDLPYKGNTEIGNDVWIGRDVTIMPVGIQNGAIIAAKSV
VTQNVDPYSVVGGNPSRLIKIRPSKEKLAALLKVRWWDLEIETINENIDC
ILNGDIKKVRS

Figure 7 (cont.)

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SEQ ID NO: 7	K S I L E N V	VgaB
SEQ ID NO: 11	1795 5'- aaa tct atc tta gaa aat gtt -3' g agc t	1815 vgaB
SEQ ID NO: 8	N Y T N Y I E Q K E	VgaB
SEQ ID NO: 12	1237 5'- aat tat aca aac tat ata gag caa aaa gaa-3' gt gtt a	1266 vgaB
SEQ ID NO: 9	I M N G A N H R M	VatC
SEQ ID NO: 13	1187 5'- ata atg aat ggg gct aat cat cgt atg -3' t t a c g	a c a a 1213 vatC
SEQ ID NO: 10	G N D V W I G	VatC
SEQ ID NO: 14	1310 a t g t 1330 5'- ggg aac gat gtt tgg att gga -3' a t a a t	vaiC

Figure 7 (cont.)

LISTE DE SÉQUENCES

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<150> US 60/050 380

<151> 1997-06-20

<160> 22

<170> PatentIn Ver. 2.2

<210> 1

<211> 1656

<212> ADN

<213> Staphylococcus

<220>

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ggcaaaacaa cactttttaa aataataaaa ggactaatag agattgacga aggaaatata 180
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caaggaatga ttaagccccc ttcaaaaaca atgggaacat ctgaatctag aatatggaaa 720
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<211> 636

<212> ADN

<213> Staphylococcus

<220>

<223> vatC

<400> 2

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tcatattacg atagtaaaga tggatgaatct tttgaaagcc aagttcttta tcaactatgaa 180
ttgattgggg ataaaactaat attaggggaag ttttgttcta ttggaccgga aacgacattt 240
ataatgaatg gggctaatac tcgtatggat ggttcaacat ttccattcaa tcttttcgga 300
aatgggtggg agaagcatac ccctacattg gaagaccttc cttataaggg taacacggaa 360
attggggaacg atgtttggat tggacgagat gtgacaatta tgcccgggtg aaaaatagga 420
aacgggggcta ttattgcagc aaaatcgggt gtgacaaaga acgttgatcc ttattcagtt 480
gttggcggta atccttcacg attaatgaag ataagggtttt ccaaggaaaa aatcgagca 540
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<211> 885

<212> ADN

<213> Staphylococcus

<220>

<223> vgbB

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tgtttaattg tatcttcact tggagacata tggtttacag agaatgggtc aaataaaatc 240
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ccttacggaa taacgggaagg tctaaatggc gatatatggt ttacccaatt gaatggagat 360
cgtataggaa agttgacagc tgatgggact atttatgaat atgatttgcc aaataagggg 420
tcttatcctg cttttattac tttaggttcg gataacgcac tttggttcac ggagaaccaa 480
aataattcta ttggaaggat tacaaataga gggaaattag aagaatatcc tctaccaaca 540
aatgcagcgg ctccagtggt tatcactagt ggtaacgatg gtgactctg gtttgtcgaa 600
attatgggca acaaaatagg tcgaatcact acaactgggt agattagcga atatgatatt 660
ccaactccaa acgcacgtcc acacgctata accgcgggga aaaaatagcga aatatggttt 720
actgaatggg gggcaaatca aatcggcaga attacaaacg acaaaaacaat tcaagaatat 780
caacttcaaa cagaaaaatgc ggaacctcat ggtattacct ttggaaaaga tggatccgta 840
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<210> 4

<211> 552

<212> PRT

<213> Staphylococcus

<220>

<223> vgaB

<400> 4

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Gly Ile Val Gly Lys Asn Gly Val Gly Lys Thr Thr Leu Leu Lys Ile
          35              40              45

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Ile Lys Gly Leu Ile Glu Ile Asp Glu Gly Asn Ile Ile Ile Ser Glu
 50 55 60
 Lys Thr Thr Ile Lys Tyr Ile Ser Gln Leu Glu Glu Pro His Ser Lys
 65 70 75 80
 Ile Ile Asp Gly Lys Tyr Ala Ser Ile Phe Gln Val Glu Asn Lys Trp
 85 90 95
 Asn Asp Asn Met Ser Gly Gly Glu Lys Thr Arg Phe Lys Leu Ala Glu
 100 105 110
 Gly Phe Gln Asp Gln Cys Ser Leu Met Leu Val Asp Glu Pro Thr Ser
 115 120 125
 Asn Leu Asp Ile Glu Gly Ile Glu Leu Ile Thr Asn Thr Phe Lys Glu
 130 135 140
 Tyr Arg Asp Thr Phe Leu Val Val Ser His Asp Arg Ile Phe Leu Asp
 145 150 155 160
 Gln Val Cys Thr Lys Ile Phe Glu Ile Glu Asn Gly Tyr Ile Arg Glu
 165 170 175
 Phe Ile Gly Asn Tyr Thr Asn Tyr Ile Glu Gln Lys Glu Met Leu Leu
 180 185 190
 Arg Lys Gln Gln Glu Glu Tyr Glu Lys Tyr Asn Ser Lys Arg Lys Gln
 195 200 205
 Leu Glu Gln Ala Ile Lys Leu Lys Glu Asn Lys Ala Gln Gly Met Ile
 210 215 220
 Lys Pro Pro Ser Lys Thr Met Gly Thr Ser Glu Ser Arg Ile Trp Lys
 225 230 235 240
 Met Gln His Ala Thr Lys Gln Lys Lys Met His Arg Asn Thr Lys Ser
 245 250 255
 Leu Glu Thr Arg Ile Asp Lys Leu Asn His Val Glu Lys Ile Lys Glu
 260 265 270
 Leu Pro Ser Ile Lys Met Asp Leu Pro Asn Arg Glu Gln Phe His Gly
 275 280 285
 Arg Asn Val Ile Ser Leu Lys Asn Leu Ser Ile Lys Phe Asn Asn Gln
 290 295 300
 Phe Leu Trp Arg Asp Ala Ser Phe Val Ile Lys Gly Gly Glu Lys Val
 305 310 315 320
 Ala Ile Ile Gly Asn Asn Gly Val Gly Lys Thr Thr Leu Leu Lys Leu
 325 330 335
 Ile Leu Glu Lys Val Glu Ser Val Ile Ile Ser Pro Ser Val Lys Ile
 340 345 350
 Gly Tyr Val Ser Gln Asn Leu Asp Val Leu Gln Ser His Lys Ser Ile
 355 360 365

Leu Glu Asn Val Met Ser Thr Ser Ile Gln Asp Glu Thr Ile Ala Arg
 370 375 380
 Ile Val Leu Ala Arg Leu His Phe Tyr Arg Asn Asp Val His Lys Glu
 385 390 395 400
 Ile Asn Val Leu Ser Gly Gly Glu Gln Ile Lys Val Ala Phe Ala Lys
 405 410 415
 Leu Phe Val Ser Asp Cys Asn Thr Leu Ile Leu Asp Glu Pro Thr Asn
 420 425 430
 Tyr Leu Asp Ile Asp Ala Val Glu Ala Leu Glu Glu Leu Leu Ile Thr
 435 440 445
 Tyr Glu Gly Val Val Leu Phe Ala Ser His Asp Lys Lys Phe Ile Gln
 450 455 460
 Asn Leu Ala Glu Gln Leu Leu Ile Ile Glu Asn Asn Lys Val Lys Lys
 465 470 475 480
 Phe Glu Gly Thr Tyr Ile Glu Tyr Leu Lys Ile Lys Asp Lys Pro Lys
 485 490 495
 Leu Asn Thr Asn Glu Lys Glu Leu Lys Glu Lys Lys Met Ile Leu Glu
 500 505 510
 Met Gln Ile Ser Ser Leu Leu Ser Lys Ile Ser Met Glu Glu Asn Glu
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 Glu Lys Asn Lys Glu Leu Asp Glu Lys Tyr Lys Leu Lys Leu Lys Glu
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 <213> Staphylococcus

<220>
 <223> vatC

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 Pro Asn Ile Leu Val Gly Glu Tyr Ser Tyr Tyr Asp Ser Lys Asp Gly
 35 40 45
 Glu Ser Phe Glu Ser Gln Val Leu Tyr His Tyr Glu Leu Ile Gly Asp
 50 55 60
 Lys Leu Ile Leu Gly Lys Phe Cys Ser Ile Gly Pro Gly Thr Thr Phe
 65 70 75 80

Ile Met Asn Gly Ala Asn His Arg Met Asp Gly Ser Thr Phe Pro Phe
85 90 95

Asn Leu Phe Gly Asn Gly Trp Glu Lys His Thr Pro Thr Leu Glu Asp
100 105 110

Leu Pro Tyr Lys Gly Asn Thr Glu Ile Gly Asn Asp Val Trp Ile Gly
115 120 125

Arg Asp Val Thr Ile Met Pro Gly Val Lys Ile Gly Asn Gly Ala Ile
130 135 140

Ile Ala Ala Lys Ser Val Val Thr Lys Asn Val Asp Pro Tyr Ser Val
145 150 155 160

Val Gly Gly Asn Pro Ser Arg Leu Ile Lys Ile Arg Phe Ser Lys Glu
165 170 175

Lys Ile Ala Ala Leu Leu Lys Val Arg Trp Trp Asp Leu Glu Ile Glu
180 185 190

Thr Ile Asn Glu Asn Ile Asp Cys Ile Leu Asn Gly Asp Ile Lys Lys
195 200 205

Val Lys Arg Ser
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<210> 6
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<212> PRT
<213> Staphylococcus

<220>
<223> vgbB

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Pro Tyr Gly Ile Thr Ser Ser Glu Asp Gly Lys Val Trp Phe Thr Gln
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His Lys Ala Asn Lys Ile Ser Ser Leu Asp Gln Ser Gly Arg Ile Lys
35 40 45

Glu Phe Glu Val Pro Thr Pro Asp Ala Lys Val Met Cys Leu Ile Val
50 55 60

Ser Ser Leu Gly Asp Ile Trp Phe Thr Glu Asn Gly Ala Asn Lys Ile
65 70 75 80

Gly Lys Leu Ser Lys Lys Gly Gly Phe Thr Glu Tyr Pro Leu Pro Gln
85 90 95

Pro Asp Ser Gly Pro Gly Ile Thr Glu Gly Leu Asn Gly Asp Ile Trp
100 105 110

Phe Thr Gln Leu Asn Gly Asp Arg Ile Gly Lys Leu Thr Ala Asp Gly

115	120	125
Thr Ile Tyr Glu Tyr Asp Leu Pro Asn Lys Gly Ser Tyr Pro Ala Phe 130 135 140		
Ile Thr Leu Gly Ser Asp Asn Ala Leu Trp Phe Thr Glu Asn Gln Asn 145 150 155 160		
Asn Ser Ile Gly Arg Ile Thr Asn Thr Gly Lys Leu Glu Glu Tyr Pro 165 170 175		
Leu Pro Thr Asn Ala Ala Ala Pro Val Gly Ile Thr Ser Gly Asn Asp 180 185 190		
Gly Ala Leu Trp Phe Val Glu Ile Met Gly Asn Lys Ile Gly Arg Ile 195 200 205		
Thr Thr Thr Gly Glu Ile Ser Glu Tyr Asp Ile Pro Thr Pro Asn Ala 210 215 220		
Arg Pro His Ala Ile Thr Ala Gly Lys Asn Ser Glu Ile Trp Phe Thr 225 230 235 240		
Glu Trp Gly Ala Asn Gln Ile Gly Arg Ile Thr Asn Asp Lys Thr Ile 245 250 255		
Gln Glu Tyr Gln Leu Gln Thr Glu Asn Ala Glu Pro His Gly Ile Thr 260 265 270		
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<220>
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<210> 8
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 <212> PRT
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<220>
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<220>
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<400> 9
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<220>
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<220>

<223> vatC

<400> 13

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27

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<211> 21

<212> ADN

<213> Staphylococcus

<220>

<223> vatC

<400> 14

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21

<210> 15

<211> 2411

<212> ADN

<213> Staphylococcus

<220>

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<222> (700)..(2355)

<220>

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<222> (2388)..(2411)

<220>

<223> vgaB et vatB

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 tagaatatga aaaagatcga aatgaaaaac tatcaaaact taacgataat ttattggaac 180
 agttagataa aaatcaaaca ttattagatc agcaacaaag attaagtctt aatgatcaaa 240
 atagtatcaa aatgtttagaa tcagaattag aagaaaaaaa gaagaaaaag aagaaaaaga 300
 aactaagtgg tatcatgtat tccagagaaa aaaataatta tatattaaaa tgagatacaa 360
 caaatgaatt agtttgtttc aataggaatt tggtaaaacc catgtacata taacttttaa 420
 tttagtataa ttaaataaac aaagaaatcg aaagggtgaa atattaataa aatgatcaaa 480
 taatccgtca ctaaaaagaa aattaaatat attggaaaga ttttacctaa tatatttatg 540
 tctattttatt atgattggat agtttgttta tttgttatat ttcacttata taaactatcc 600
 tctatttttaa aaaaaggagg atttttttat gcttttgttt atttgttata tttcacttat 660
 ataaactatc ctctatttta aaaaaaggag gattttttt atg ctt aaa atc gac 714

Met Leu Lys Ile Asp

atg aag aat gta aaa aaa tat tat gca gat aaa tta att tta aat ata	762
Met Lys Asn Val Lys Lys Tyr Tyr Ala Asp Lys Leu Ile Leu Asn Ile	
10 15 20	
aaa gaa cta aag att tat agt ggg gat aaa ata ggt att gta ggt aag	810
Lys Glu Leu Lys Ile Tyr Ser Gly Asp Lys Ile Gly Ile Val Gly Lys	
25 30 35	
aat gga gtt ggc aaa aca aca ctt tta aaa ata ata aaa gga cta ata	858
Asn Gly Val Gly Lys Thr Thr Leu Leu Lys Ile Ile Lys Gly Leu Ile	
40 45 50	
gag att gac gaa gga aat ata att ata agt gaa aaa aca act att aaa	906
Glu Ile Asp Glu Gly Asn Ile Ile Ile Ser Glu Lys Thr Thr Ile Lys	
55 60 65	
tat atc tct caa tta gaa gaa cca cat agt aag ata att gat gga aaa	954
Tyr Ile Ser Gln Leu Glu Glu Pro His Ser Lys Ile Ile Asp Gly Lys	
70 75 80 85	
tat gct tca ata ttt caa gtt gaa aat aag tgg aat gac aat atg agt	1002
Tyr Ala Ser Ile Phe Gln Val Glu Asn Lys Trp Asn Asp Asn Met Ser	
90 95 100	
ggt ggt gaa aaa act aga ttt aaa cta gca gag gga ttt caa gat caa	1050
Gly Gly Glu Lys Thr Arg Phe Lys Leu Ala Glu Gly Phe Gln Asp Gln	
105 110 115	
tgt tct tta atg ctc gta gat gaa cct aca agt aat tta gat atc gaa	1098
Cys Ser Leu Met Leu Val Asp Glu Pro Thr Ser Asn Leu Asp Ile Glu	
120 125 130	
gga ata gag ttg ata aca aat act ttt aaa gag tac cgt gat act ttt	1146
Gly Ile Glu Leu Ile Thr Asn Thr Phe Lys Glu Tyr Arg Asp Thr Phe	
135 140 145	
ttg gta gta tct cat gat aga att ttt tta gat caa gtt tgt aca aaa	1194
Leu Val Val Ser His Asp Arg Ile Phe Leu Asp Gln Val Cys Thr Lys	
150 155 160 165	
att ttt gaa att gaa aat gga tat att aga gaa ttc atc ggt aat tat	1242
Ile Phe Glu Ile Glu Asn Gly Tyr Ile Arg Glu Phe Ile Gly Asn Tyr	
170 175 180	
aca aac tat ata gag caa aaa gaa atg ctt cta cga aag caa caa gaa	1290
Thr Asn Tyr Ile Glu Gln Lys Glu Met Leu Leu Arg Lys Gln Gln Glu	
185 190 195	
gaa tac gaa aag tat aat tct aaa aga aag caa ttg gag caa gct ata	1338
Glu Tyr Glu Lys Tyr Asn Ser Lys Arg Lys Gln Leu Glu Gln Ala Ile	
200 205 210	
aag cta aaa gag aat aag gcg caa gga atg att aag ccc cct tca aaa	1386
Lys Leu Lys Glu Asn Lys Ala Gln Gly Met Ile Lys Pro Pro Ser Lys	
215 220 225	
aca atg gga aca tct gaa tct aga ata tgg aaa atg caa cat gct act	1434
Thr Met Gly Thr Ser Glu Ser Arg Ile Trp Lys Met Gln His Ala Thr	
230 235 240 245	

aaa caa aaa aag atg cat aga aat acg aaa tcg ttg gaa aca cga ata	1482
Lys Gln Lys Lys Met His Arg Asn Thr Lys Ser Leu Glu Thr Arg Ile	
250 255 260	
gat aaa tta aat cat gta gaa aaa ata aaa gag ctt cct tct att aaa	1530
Asp Lys Leu Asn His Val Glu Lys Ile Lys Glu Leu Pro Ser Ile Lys	
265 270 275	
atg gat tta cct aat aga gag caa ttt cat ggt cgc aat gta att agt	1578
Met Asp Leu Pro Asn Arg Glu Gln Phe His Gly Arg Asn Val Ile Ser	
280 285 290	
tta aaa aac tta tct ata aaa ttt aat aat caa ttt ctt tgg aga gat	1626
Leu Lys Asn Leu Ser Ile Lys Phe Asn Asn Gln Phe Leu Trp Arg Asp	
295 300 305	
gct tca ttt gtc att aaa ggt gga gaa aag gtt gct ata att ggt aac	1674
Ala Ser Phe Val Ile Lys Gly Gly Glu Lys Val Ala Ile Ile Gly Asn	
310 315 320 325	
aat ggt gta gga aaa aca aca ttg ttg aag ctg att cta gaa aaa gta	1722
Asn Gly Val Gly Lys Thr Thr Leu Leu Lys Leu Ile Leu Glu Lys Val	
330 335 340	
gaa tca gta ata ata tca cca tca gtt aaa att gga tac gtc agt caa	1770
Glu Ser Val Ile Ile Ser Pro Ser Val Lys Ile Gly Tyr Val Ser Gln	
345 350 355	
aac tta gat gtt cta caa tct cat aaa tct atc tta gaa aat gtt atg	1818
Asn Leu Asp Val Leu Gln Ser His Lys Ser Ile Leu Glu Asn Val Met	
360 365 370	
tct acc tcc att caa gat gaa aca ata gca aga att gtt cta gca aga	1866
Ser Thr Ser Ile Gln Asp Glu Thr Ile Ala Arg Ile Val Leu Ala Arg	
375 380 385	
tta cat ttt tat cgc aat gat gtt cat aaa gaa ata aat gtt ttg agt	1914
Leu His Phe Tyr Arg Asn Asp Val His Lys Glu Ile Asn Val Leu Ser	
390 395 400 405	
ggt gga gaa caa ata aag gtt gct ttt gcc aag cta ttt gtt agc gat	1962
Gly Gly Glu Gln Ile Lys Val Ala Phe Ala Lys Leu Phe Val Ser Asp	
410 415 420	
tgt aat aca tta att ctt gat gaa cca aca aac tat ttg gat atc gat	2010
Cys Asn Thr Leu Ile Leu Asp Glu Pro Thr Asn Tyr Leu Asp Ile Asp	
425 430 435	
gct gtt gag gca tta gaa gaa ttg tta att acc tat gaa ggt gtt gtg	2058
Ala Val Glu Ala Leu Glu Glu Leu Leu Ile Thr Tyr Glu Gly Val Val	
440 445 450	
tta ttt gct tcc cat gat aaa aaa ttt ata caa aac cta gct gaa caa	2106
Leu Phe Ala Ser His Asp Lys Lys Phe Ile Gln Asn Leu Ala Glu Gln	
455 460 465	
ttg tta ata ata gaa aat aat aaa gtg aaa aaa ttc gaa gga aca tat	2154
Leu Leu Ile Ile Glu Asn Asn Lys Val Lys Lys Phe Glu Gly Thr Tyr	
470 475 480 485	
ata gaa tat tta aaa att aaa gat aaa cca aaa tta aat aca aat gaa	2202

Ile	Glu	Tyr	Leu	Lys	Ile	Lys	Asp	Lys	Pro	Lys	Leu	Asn	Thr	Asn	Glu	
				490					495					500		
aaa	gaa	ctc	aaa	gaa	aaa	aag	atg	ata	cta	gaa	atg	caa	att	tca	tca	2250
Lys	Glu	Leu	Lys	Glu	Lys	Lys	Met	Ile	Leu	Glu	Met	Gln	Ile	Ser	Ser	
			505					510					515			
tta	tta	agt	aaa	atc	tca	atg	gaa	gaa	aat	gaa	gaa	aaa	aac	aaa	gaa	2298
Leu	Leu	Ser	Lys	Ile	Ser	Met	Glu	Glu	Asn	Glu	Glu	Lys	Asn	Lys	Glu	
			520				525					530				
tta	gat	gaa	aag	tac	aaa	ttg	aaa	tta	aaa	gaa	ttg	aaa	agc	cta	aat	2346
Leu	Asp	Glu	Lys	Tyr	Lys	Leu	Lys	Leu	Lys	Glu	Leu	Lys	Ser	Leu	Asn	
	535					540					545					
aaa	aat	att	taaaataaat	tatattaata	ggaggttttaa	aa	atg	aaa	tat	ggc						2399
Lys	Asn	Ile							Met	Lys	Tyr	Gly				
550											555					
cct	gat	cca	aat													2411
Pro	Asp	Pro	Asn													
			560													

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 <213> Staphylococcus

<220>
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 <222> (39)..(926)

<220>
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<220>
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gag	ttt	aac	ttg	tct	att	ccc	gat	tca	ggt	cca	tac	ggt	ata	act	tca	104
Glu	Phe	Asn	Leu	Ser	Ile	Pro	Asp	Ser	Gly	Pro	Tyr	Gly	Ile	Thr	Ser	
			10					15					20			

tca	gaa	gac	gga	aag	gta	tgg	ttc	aca	caa	cat	aag	gca	aac	aaa	atc	152
Ser	Glu	Asp	Gly	Lys	Val	Trp	Phe	Thr	Gln	His	Lys	Ala	Asn	Lys	Ile	
			25				30					35				

agc	agt	cta	gat	cag	agt	ggt	agg	ata	aaa	gaa	ttc	gaa	gtt	cct	acc	200
Ser	Ser	Leu	Asp	Gln	Ser	Gly	Arg	Ile	Lys	Glu	Phe	Glu	Val	Pro	Thr	
		40				45					50					

cct	gat	gct	aaa	gtg	atg	tgt	tta	att	gta	tct	tca	ctt	gga	gac	ata	248
Pro	Asp	Ala	Lys	Val	Met	Cys	Leu	Ile	Val	Ser	Ser	Leu	Gly	Asp	Ile	
		55			60					65					70	

tgg ttt aca gag aat ggt gca aat aaa atc gga aag ctc tca aaa aaa	296
Trp Phe Thr Glu Asn Gly Ala Asn Lys Ile Gly Lys Leu Ser Lys Lys	
75 80 85	
ggt ggc ttt aca gaa tat cca ttg cca cag ccg gat tct ggt cct tac	344
Gly Gly Phe Thr Glu Tyr Pro Leu Pro Gln Pro Asp Ser Gly Pro Tyr	
90 95 100	
gga ata acg gaa ggt cta aat ggc gat ata tgg ttt acc caa ttg aat	392
Gly Ile Thr Glu Gly Leu Asn Gly Asp Ile Trp Phe Thr Gln Leu Asn	
105 110 115	
gga gat cgt ata gga aag ttg aca gct gat ggg act att tat gaa tat	440
Gly Asp Arg Ile Gly Lys Leu Thr Ala Asp Gly Thr Ile Tyr Glu Tyr	
120 125 130	
gat ttg cca aat aag gga tct tat cct gct ttt att act tta ggt tcg	488
Asp Leu Pro Asn Lys Gly Ser Tyr Pro Ala Phe Ile Thr Leu Gly Ser	
135 140 145 150	
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Asp Asn Ala Leu Trp Phe Thr Glu Asn Gln Asn Asn Ser Ile Gly Arg	
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Ile Thr Asn Thr Gly Lys Leu Glu Glu Tyr Pro Leu Pro Thr Asn Ala	
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Ala Ala Pro Val Gly Ile Thr Ser Gly Asn Asp Gly Ala Leu Trp Phe	
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Val Glu Ile Met Gly Asn Lys Ile Gly Arg Ile Thr Thr Thr Gly Glu	
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Ile Ser Glu Tyr Asp Ile Pro Thr Pro Asn Ala Arg Pro His Ala Ile	
215 220 225 230	
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Thr Ala Gly Lys Asn Ser Glu Ile Trp Phe Thr Glu Trp Gly Ala Asn	
235 240 245	
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Gln Ile Gly Arg Ile Thr Asn Asp Lys Thr Ile Gln Glu Tyr Gln Leu	
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Gln Thr Glu Asn Ala Glu Pro His Gly Ile Thr Phe Gly Lys Asp Gly	
265 270 275	
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Ser Val Trp Phe Ala Leu Lys Cys Lys Ile Gly Lys Leu Asn Leu Asn	
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Glu Met Lys Trp Gln Asn Gln Gln Gly Pro	
295 300 305	
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Asn Pro Glu Glu Ile Tyr Pro Ile Glu Gly Asn Lys His Val Gln Phe	
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Ile Lys Pro Ser Ile Thr Lys Pro Asn Ile Leu Val Gly Glu Tyr Ser	
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Tyr Tyr Asp Ser Lys Asp Gly Glu Ser Phe Glu Ser Gln Val Leu Tyr	
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His Tyr Glu Leu Ile Gly Asp Lys Leu Ile Leu Gly Lys Phe Cys Ser	
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Ile Gly Pro Gly Thr Thr Phe Ile Met Asn Gly Ala Asn His Arg Met	
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Asp Gly Ser Thr Phe Pro Phe Asn Leu Phe Gly Asn Gly Trp Glu Lys	
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His Thr Pro Thr Leu Glu Asp Leu Pro Tyr Lys Gly Asn Thr Glu Ile	
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Gly Asn Asp Val Trp Ile Gly Arg Asp Val Thr Ile Met Pro Gly Val	
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Lys Ile Gly Asn Gly Ala Ile Ile Ala Ala Lys Ser Val Val Thr Lys	
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Asn Val Asp Pro Tyr Ser Val Val Gly Gly Asn Pro Ser Arg Leu Ile	
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